

OY 3 GYKNSKF 9  
| | : |  
Db 1 GUGNNAF 7

## RESULT 20

GRAR\_RANRU STANDARD; PRT; 12 AA.

AC P40754;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Granuliberin-R.  
OS Rana rugosa (Wrinkled frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OX NCBI\_TaxID=8410;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=78062810; PubMed=589733;  
RA Nakajima T., Yasuhara T.;  
RT "A new mast cell degranulating peptide, granuliberin-R, in the frog  
RT (Rana rugosa) skin.";  
RL Chem. Pharm. Bull. 25:2464-2465(1977).  
RN [2]  
RP SYNTHESIS.  
RX MEDLINE=78189201; PubMed=657408;  
RA Nakajima T., Yasuhara T., Hirai Y., Kitada C., Fujino M., Takeyama M.,  
RA Koyama K., Yajima H.;  
RT "Synthesis of the dodecapeptide amide corresponding to the entire  
RT amino acid sequence of granuliberin-R, a new frog skin peptide from  
RT Rana rugosa.";  
RL Chem. Pharm. Bull. 26:1222-1230(1978).  
CC -1- FUNCTION: Mast cell degranulating peptide.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Mast cell degranulation; Amidation.  
FT MOD\_RES 12 12 AMIDATION.  
SQ SEQUENCE 12 AA; 1424 MW; 2B974EB9CA1B5047 CRC64;

Query Match 29.4%; Score 15; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 5.5e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 FGy 4  
| | : |  
Db 1 FGF 3

## RESULT 21

NP1\_LYMST STANDARD; PRT; 13 AA.

AC P80178;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-JUL-1993 (Rel. 26, Last annotation update)  
DE Lytna-Df-amide 1.  
OS Lymnaea stagnalis (Great pond snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
OC Lymnaeidae; Lymnaeidae; Lymnaea.  
OX NCBI\_TaxID=6523;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RX MEDLINE=93238777; PubMed=8477756;  
RA Johnsen A.H., Rehfeld J.F.;  
RT "Lymnaeidae, a new family of neuropeptides from the pond snail,  
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in  
RT invertebrates?";  
RL Eur. J. Biochem. 213:875-879(1993).  
CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.

DR PIR; S32471; S32471.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 13 13 AMIDATION.  
SQ SEQUENCE 13 AA; 1519 MW; 9CA07BA3F5D5B455 CRC64;

Query Match 29.4%; Score 15; DB 1; Length 13;  
Best Local Similarity 75.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 NSKF 9  
| | : |  
Db 7 NSAF 10

## RESULT 22

NP4\_LYMST STANDARD; PRT; 13 AA.

AC P80181;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-JUL-1993 (Rel. 26, Last annotation update)  
DE Lytna-Df-amide 4.  
OS Lymnaea stagnalis (Great pond snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
OC Lymnaeidae; Lymnaeidae; Lymnaea.  
OX NCBI\_TaxID=6523;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RX MEDLINE=93238777; PubMed=8477756;  
RA Johnsen A.H., Rehfeld J.F.;  
RT "Lymnaeidae, a new family of neuropeptides from the pond snail,  
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in  
RT invertebrates?";  
RL Eur. J. Biochem. 213:875-879(1993).  
CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.  
DR PIR; S32474; S32474.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 13 13 AMIDATION.  
SQ SEQUENCE 13 AA; 1503 MW; 9CA07BBB56D5B455 CRC64;

Query Match 29.4%; Score 15; DB 1; Length 13;  
Best Local Similarity 75.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 NSKF 9  
| | : |  
Db 7 NSAF 10

## RESULT 23

TEML\_RANTE STANDARD; PRT; 13 AA.

AC P57104;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Temporin L.  
OS Rana temporaria (European common frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OX NCBI\_TaxID=8407;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=97175050; PubMed=9022710;  
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,  
RA Barra D.;  
RT "Temporins, antimicrobial peptides from the European red frog Rana  
RT temporaria.";  
RL Eur. J. Biochem. 242:788-792(1996).  
CC -1- FUNCTION: Has antibacterial activity against Gram-negative and  
CC Gram-positive bacteria.

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CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the breviniin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1641 MW; 9EBDCB1FAFF7C325 CRC64;

Query Match
Best Local Similarity 29.4%; Score 15; DB 1; Length 13;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SKP 9
DB 6 SKP 8

RESULT 24
MY14_EISFO STANDARD; PRT; 14 AA.
ID MY14_EISFO
AC P46979;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myoactive tetradecapeptide (ETP).
OS Eisenia foetida (Common brandling worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Gut;
RX MEDLINE=96087879; PubMed=8532604;
RA Ukena K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "A novel gut tetradecapeptide isolated from the earthworm, Eisenia
foetida."
RL Peptides 16:995-999(1995).
CC -!- FUNCTION: Has a stimulative effect on the contraction of gut
muscles.
CC -!- SIMILARITY: TO INSECTS ALLATOTROPIN.
KW Neuropeptide; Amidation.
FT MOD_RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA; 1478 MW; CC9ABEF941CD91AD CRC64;

Query Match
Best Local Similarity 29.4%; Score 15; DB 1; Length 14;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKN 6
DB 1 GFKD 4

RESULT 25
RS19_PPWBP STANDARD; PRT; 14 AA.
ID RS19_PPWBP
AC Q52093;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS19.
OS Pigeon pea witches'-broom phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.
OX NCBI_TaxID=37700;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
their classification."
RL J. Bacteriol. 176:5244-5254(1994);
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CC -!- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
CC to the 16S ribosomal RNA (By similarity).
CC -!- SIMILARITY: Belongs to the S19P family of ribosomal proteins.
CC -----
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CC -----
DR EMBL; L27036; AAA83946.1; -
DR HAMAP; MF_00531; -; 1.
DR InterPro; IPR002222; Ribosomal S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1668 MW; 8FD46F6B830DFBBA CRC64;

Query Match
Best Local Similarity 29.4%; Score 15; DB 1; Length 14;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KNSK 8
DB 6 KDSK 9

RESULT 26
SMS1_MYOSC STANDARD; PRT; 14 AA.
ID SMS1_MYOSC
AC P20750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin I.
OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin),
OS Oncochrychus kisutch (Coho salmon), and
OS Anguilla anguilla (European freshwater eel).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottidae; Cottidae; Myoxocephalus.
OX NCBI_TaxID=8097, 8019, 7936;
RN [1]
RP SEQUENCE.
RC SPECIES=M.scorpius; TISSUE=Pancreas;
RX MEDLINE=88029486; PubMed=2889597;
RA Conlon J.M., Davis M.S., Falkner S., Thim L.;
RT "Structural characterization of peptides derived from
prosomatostatin I and II isolated from the pancreatic islets of two
species of teleostean fish: the daddy sculpin and the flounder."
RL Eur. J. Biochem. 168:647-652(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=O.kisutch; TISSUE=Pancreas;
RX MEDLINE=87055212; PubMed=2877919;
RA Plisetskaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,
RA Kimmel J.R., Andrews P.C., Gorman A.;
RT "Characterization of coho salmon (Oncochrychus kisutch) islet
somatostatin."
RL Gen. Comp. Endocrinol. 63:252-263(1986).
RN [3]
RP SEQUENCE.
RC SPECIES=A.anguilla; TISSUE=Pancreas;
RX MEDLINE=89065329; PubMed=2904391;
RA Conlon J.M., Deacon C.F., Hazon N., Henderson I.W., Thim L.;
RT "Somatostatin-related and glucagon-related peptides with unusual
structural features from the European eel (Anguilla anguilla).";
RL Gen. Comp. Endocrinol. 72:181-189(1988).
CC -!- FUNCTION: Somatostatin inhibits the release of somatotropin.
CC -!- SUBCELLULAR LOCATION: Secreted.
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CC -1- SIMILARITY: Belongs to the somatostatin family.
DR PIR; A60840; A60840.
OS PIR; B60842; B60842.
DR PIR; S00172; S00172.
DR InterPro; IPR004250; Somatostatin.
DR Pfam; PF03002; Somatostatin; 1.
KM Hormone; Multigene family.
FT DISULFID 3 14
SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match
Best Local Similarity 29.4%; Score 15; DB 1; Length 14;
Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKN 6
Db 2 GCKN 5

RESULT 27
SMS_ALIMI STANDARD; PRT; 14 AA.
ID SMS_ALIMI
AC P31885;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin-14.
OS Alligator mississippiensis (American alligator), and
OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496, 34903;
RN [1]
RP SEQUENCE.
RC SPECIES=A.mississippiensis; TISSUE=Stomach;
RX MEDLINE=93324451; PubMed=8101369;
RA Wang Y., Conlon J.M.;
RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
RT and stomach of the alligator.";
RL Peptides 14:573-579(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=T.scripta;
RX MEDLINE=90341082; PubMed=1974347;
RA Conlon J.M., Hicks J.W.;
RT "Isolation and structural characterization of insulin, glucagon and
RT somatostatin from the turtle, Pseudemys scripta.";
RL Peptides 11:461-466(1990).
CC -1- FUNCTION: Somatostatin inhibits the release of somatotropin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the somatostatin family.
DR PIR; C60414; C60414.
DR InterPro; IPR004250; Somatostatin.
DR Pfam; PF03002; Somatostatin; 1.
KM Hormone.
FT DISULFID 3 14
SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match
Best Local Similarity 29.4%; Score 15; DB 1; Length 14;
Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKN 6
Db 2 GCKN 5

RESULT 28
LCK5_LEUMA STANDARD; PRT; 8 AA.
ID LCK5_LEUMA
AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
RT myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach protoderm (hindgut).
CC -1- SUBCELLULAR LOCATION: Secreted.
DR PIR; J50315; J50315.
DR PIR; J50315; J50315.
KM Neuropeptide; Amidation.
FT MOD RES 8 8
SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match
Best Local Similarity 27.5%; Score 14; DB 1; Length 8;
Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKN 6
Db 1 GSGFSS 6

RESULT 29
SAMP_MUSCA STANDARD; PRT; 9 AA.
ID SAMP_MUSCA
AC P19095;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum amyloid P-component (SAP) (Fragment).
OS Mustelus canis (Smooth dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
OC Mustelus.
OX NCBI_TaxID=7812;
RN [1]
RP SEQUENCE.
RX MEDLINE=83160932; PubMed=6403520;
RA Robey F.A., Tanaka T., Liu T.-Y.;
RT "Isolation and characterization of two major serum proteins from the
RT dogfish, Mustelus canis, C-reactive protein and amyloid P
RT component.";
RL J. Biol. Chem. 258:3889-3894(1983).
CC -1- SUBUNIT: Homopentamer. Pentaxin (or pentraxin) have a discoid
CC arrangement of 5 noncovalently bound subunits.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC -1- SIMILARITY: Belongs to the pentaxin family.
DR PIR; B20569; B20569.
DR InterPro; IPR001759; Pentaxin.
DR PROSITE; PS00289; PENTAXIN; PARTIAL.
KM Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
FT DOMAIN 1 9
FT NON TER 9 9
SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match
Best Local Similarity 27.5%; Score 14; DB 1; Length 9;
Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYKSKF 9

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Db 1 GFPKSLIF 9

RESULT 30  
FAR2\_PENMO STANDARD; PRT; 10 AA.  
ID FAR2\_PENMO  
AC P83317;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRamide-like neuropeptide FLP2 (AYSNLYLRF-amide).  
OS Pennaeus monodon (Penaeid shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeidea; Penaeidae; Pennaeus.  
OX NCBI\_TaxID=6687;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RX MEDLINE=21956277; PubMed=11959015;  
RA Sithigorngul P., Pupuem U., Krungkaseem C., Longyant S., Chaitvutthangkura P., Sithigorngul W., Petsom A.;  
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk of the giant tiger prawn Pennaeus monodon."  
RL Comp. Biochem. Physiol. 131B:325-337(2002).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- MASS SPECTROMETRY: MW=1260.0; METHOD=MALDI.  
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide) family.  
DR GO:0007218; P:neuropeptide signaling pathway; TAS.  
KW Neuropeptide; Amidation.  
FT MOD RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1260 MW; 88F9023B54472455 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 10;  
Best Local Similarity 33.3%; Pred. No. 7e+03;  
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YKNSKF 9  
Db 2 YSNLNY 7

RESULT 31  
RL16\_ACHLA STANDARD; PRT; 10 AA.  
ID RL16\_ACHLA  
AC P29221;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE 50S ribosomal protein L16 (Fragment).  
GN RPLP.  
OS Acholeplasma laidlawi.  
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales; OC Acholeplasmataceae; Acholeplasma.  
OX NCBI\_TaxID=2148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92210505; PubMed=1556079;  
RA Lim P.O., Sears B.B.;  
RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like organism and Acholeplasma laidlawi deduced from two ribosomal protein gene sequences."  
RL J. Bacteriol. 174:2606-2611(1992).  
CC -1- FUNCTION: This protein binds directly to 23S ribosomal RNA and is located at the site of the peptidyltransferase center (By similarity).  
CC -1- SIMILARITY: Belongs to the L16P family of ribosomal proteins.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: M74771; AAA21914.1; .  
DR PIR: F41839; F41839.  
DR InterPro: IPR000114; Ribosomal\_L16.  
DR PROSITE: PS00586; RIBOSOMAL\_L16\_1; PARTIAL.  
DR PROSITE: PS00701; RIBOSOMAL\_L16\_2; PARTIAL.  
KW Ribosomal protein; rRNA-binding.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1324 MW; B3386A21B4032766 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 10;  
Best Local Similarity 40.0%; Pred. No. 7e+03;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 KNSKF 9  
Db 5 KRTXY 9

RESULT 32  
EFG\_CLOPA STANDARD; PRT; 11 AA.  
ID EFG\_CLOPA  
AC P81350;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Elongation factor G (EF-G) (CP 5) (Fragment).  
GN FUSA.  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; OC Clostridium.  
OX NCBI\_TaxID=1501;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W5;  
RX MEDLINE=98291870; PubMed=9629918;  
RA Flengsrud R., Skjeldal L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5."  
RL Electrophoresis 19:802-806(1998).  
CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of the nascent protein chain from the A-site to the P-site of the ribosome.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.  
CC EF-G/EF-2 subfamily.  
DR InterPro: IPR00795; EF\_GTPbind.  
DR PROSITE: PS00301; EFATOR\_GTP; PARTIAL.  
KW Elongation factor; Protein biosynthesis; GTP-binding.  
FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 11;  
Best Local Similarity 50.0%; Pred. No. 7e+03;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YKNSKF 9  
Db 2 YPLEKF 7

RESULT 33  
RS19\_CLYEP STANDARD; PRT; 12 AA.  
ID RS19\_CLYEP  
AC Q46490;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 30S ribosomal protein S19 (Fragment).  
GN RPS19 OR RPS19.



```

OS Clover yellow edge phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.
OX NCBI_TaxID=35775;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
RT their classification."
RL J. Bacteriol. 176:5244-5254(1994).
CC -1- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
CC to the 16S ribosomal RNA (By similarity).
CC -1- SIMILARITY: Belongs to the S19P family of ribosomal proteins.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR HAMAP; MF_00531; -.
DR InterPro; IPR002222; Ribosomal S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1409 MW; 4CC478EFC8333AA3 CRC64;

Query Match
Best Local Similarity 27.5%; Score 14; DB 1; Length 12;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYKNSK 8
| | |
| : |
Db 1 GHAKKDKK 8

RESULT 34.
RS19_TOBBP
ID RS19_TOBBP STANDARD; PRT; 12 AA.
AC Q56251;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS19 OR RPS19.
OS Tomato big bud phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.
OX NCBI_TaxID=35770;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
RT their classification."
RL J. Bacteriol. 176:5244-5254(1994).
CC -1- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
CC to the 16S ribosomal RNA (By similarity).
CC -1- SIMILARITY: Belongs to the S19P family of ribosomal proteins.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L27004; AAA83952.1; -.

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```

DR HAMAP; MF_00531; -.
DR InterPro; IPR002222; Ribosomal S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1470 MW; 4CC88BE908333AA3 CRC64;

Query Match
Best Local Similarity 27.5%; Score 14; DB 1; Length 12;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYKNSK 8
| | |
| : |
Db 1 GHAKKDKK 8

RESULT 35
IDHC_PIG
ID IDHC_PIG STANDARD; PRT; 13 AA.
AC P20304;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1.1.1.42)
DE (Oxalosuccinate decarboxylase) (IDH) (NADP+-specific IDH) (IDP)
DE (Fragment).
GN IDH1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=87308293; PubMed=2887570;
RA Bailey J.M., Colman R.F.;
RT "Isolation of the glutamyl peptide labeled by the nucleotide analogue
RT 2-(4-bromo-2,3-dioxobutylthio)-1,N(6)-ethencadenosine
RT 2',5'-biphosphate in the active site of NADP+-specific isocitrate
RT dehydrogenase."
RL J. Biol. Chem. 262:12620-12626(1987).
RN [2]
RP SEQUENCE.
RX MEDLINE=87308292; PubMed=3624273;
RA Ehrlich R.S., Colman R.F.;
RT "Characterization of an active site peptide modified by the substrate
RT analogue 3-bromo-2-ketoglutarate on a single chain of dimeric NADP+-
RT dependent isocitrate dehydrogenase."
RL J. Biol. Chem. 262:12614-12619(1987).
CC -1- CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2)
CC + NADPH.
CC -1- SUBUNIT: Homodimer.
CC InterPro; IPR001804; Isoch.
DR PROSITE; PS00470; IDH_IMDH; PARTIAL.
KW Oxidoreductase; NADP; Tricarboxylic acid cycle.
FT ACT_SITE 1
FT NON_TER 1
FT ACT_SITE 5
FT NON_TER 5
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1353 MW; 1B640F0E9F7C71E0 CRC64;

Query Match
Best Local Similarity 27.5%; Score 14; DB 1; Length 13;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GYKNSK 8
| | |
| : |
Db 8 GLSNVK 13

RESULT 36
NEUT_CAVPO
ID NEUT_CAVPO STANDARD; PRT; 13 AA.
AC P32560;
DT 01-OCT-1993 (Rel. 27, Created)

```

DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
GN Neurotensin (NT).  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Small intestine;  
RX MEDLINE=86248085; PubMed=3087775;  
RA Shaw C., Thim L., Conlon J.M.;  
RT "Isolation of neurotensin: isolation from guinea pig intestine.";  
RL FEBS Lett. 202:187-192(1986).  
CC - FUNCTION: Smooth muscle-contracting peptide.  
CC - SUBCELLULAR LOCATION: Secreted.  
CC - SIMILARITY: Belongs to the neurotensin family.  
DR PIR; A53608; A53608.  
KW Vasoactive; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 13 AA; 1680 MW; 4C8314644C4115B3 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 13;  
Best Local Similarity 66.7%; Pred. No. 9e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 YKN 6  
|:|  
DB 3 YEN 5

## RESULT 37

UC18\_MAIZE  
ID UC18\_MAIZE STANDARD; PRT; 14 AA.

AC P80624;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 263)  
DE (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Coleoptile;  
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RA Perrotlet J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated  
genome analysis program."  
RL Theor. Appl. Genet. 93:997-1005(1996).  
CC - MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
protein is: 6.1, its MW is: 50.3 kDa.  
DR Maize-2DPAGE; P80624; COLEOPTILE.  
KW MaizeDB; 123950;  
FT NON\_TER 1  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1485 MW; 2EF9116472A39458 CRC64;

Query Match 27.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 50.0%; Pred. No. 9.7e+03;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 FGYNK 7  
|:|  
DB 9 FGIHTS 14

## RESULT 38

SAZA\_ONCMY

ID SAZA\_ONCMY STANDARD; PRT; 13 AA.

AC P82238;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Salmocidin 2A (Fragment).  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protactanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE, AND FUNCTION.

RC TISSUE=Serum;  
RA Henry M.A., Secombes C.J.;  
RT "Purification and partial characterization of antibacterial peptides  
from rainbow trout, Oncorhynchus mykiss."  
RL Submitted (DEC-1999) to Swiss-Prot.  
CC - FUNCTION: Antibacterial activity against Gram-negative bacteria.  
CC - SUBCELLULAR LOCATION: Secreted.  
CC - TISSUE SPECIFICITY: Plasma serum.  
KW Antibiotic.  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1416 MW; 5FFB792AFC645873 CRC64;

Query Match 26.5%; Score 13.5; DB 1; Length 13;  
Best Local Similarity 57.1%; Pred. No. 1.1e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

OY 1 GF--GY 4  
|:|  
DB 2 GFVLKGY 8

## RESULT 39

SA2B\_ONCMY  
ID SA2B\_ONCMY STANDARD; PRT; 13 AA.

AC P82239;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Salmocidin 2B (Fragment).  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protactanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE, AND FUNCTION.

RC TISSUE=Serum;  
RA Henry M.A., Secombes C.J.;  
RT "Purification and partial characterization of antibacterial peptides  
from rainbow trout, Oncorhynchus mykiss."  
RL Submitted (DEC-1999) to Swiss-Prot.  
CC - FUNCTION: Antibacterial activity against Gram-negative bacteria.  
CC - SUBCELLULAR LOCATION: Secreted.  
CC - TISSUE SPECIFICITY: Plasma serum.  
KW Antibiotic.  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1400 MW; 5FFB792AEBE5873 CRC64;

Query Match 26.5%; Score 13.5; DB 1; Length 13;  
Best Local Similarity 57.1%; Pred. No. 1.1e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

OY 1 GF--GY 4  
|:|  
DB 2 GFVLKGY 8

## RESULT 40

ALLS\_CYDPO

ID ALLS\_CYDPO STANDARD; PRT; 8 AA.

AC P82156;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydia statin 5.  
OS Cydia pomonella (Coddling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily.";  
RL Peptides 18:1301-1309(1997).  
CC -!- SIMILARITY: Belongs to the allatostatin family.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 8  
SQ SEQUENCE 8 AA; 898 MW; 922879CAB58640D CRC64;

Query Match 25.5%; Score 13; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GY 4  
Db 3 GY 4

RESULT 41  
NEF\_HV128  
ID NEF\_HV128 STANDARD; PRT; 9 AA.  
AC P12481;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Negative factor (F-protein) (27 kDa protein) (3'ORF) (Fragment).  
GN NEF.  
OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11681;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88281278; PubMed=3395517;  
RA Youno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,  
RA Gallo R.C.;  
RT "Nucleotide sequence analysis of the env gene of a new Zairian  
RT isolate of HIV-1.";  
RL AIDS Res. Hum. Retroviruses 4:165-173(1988).  
CC -!- FUNCTION: NEF has GTPase, GTP-binding and autophosphorylating  
CC activities. It seems to down-regulate the CD4(T4) antigen.  
CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD  
CC ZAIREAN MALE.  
CC -----  
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CC -----  
CC EMBL: J03653; AAA44687.1; -.  
DR HIV; J03653; NEFSJY1.  
KW AIDS; Myristate; GTP-binding; Lipoprotein.  
FT LIPID 2  
FT N-myristoyl glycine (in host) (By  
FT similarity).  
FT NON TER 9  
SQ SEQUENCE 9 AA; 967 MW; 319CB325A3733878 CRC64;

Query Match 25.5%; Score 13; DB 1; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GYNSK 8  
Db 2 GGYNSK 7

RESULT 42  
NEU\_CAVPO  
ID NEU\_CAVPO STANDARD; PRT; 9 AA.  
AC P34966;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuromedin U-9 (Nmu-9).  
GN Nmu.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathu; Cavidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Small intestine;  
RX MEDLINE=90341105; PubMed=2381877;  
RA Murphy R., Turner C.A., Furness J.B., Parker L., Giraud A.;  
RT "Isolation and microsequence analysis of a novel form of neuromedin U  
RT from guinea pig small intestine.";  
RL Peptides 11:613-617(1990).  
CC -!- FUNCTION: Stimulates uterine smooth muscle contraction and causes  
CC selective vasoconstriction.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the Nmu family.  
DR InterPro; IPR008199; NMu.  
DR Pfam; PF02070; NMu; 1.  
KW PROSITE; PS00967; NMu; 1.  
KW Amidation; Hormone.  
FT MOD\_RES 9  
FT SEQUENCE 9 AA; 1169 MW; 1ECF177409C729DB CRC64;

Query Match 25.5%; Score 13; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GY 4  
Db 1 GY 2

RESULT 43  
NSK1\_SARBU  
ID NSK1\_SARBU STANDARD; PRT; 9 AA.  
AC P41492;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Neosulfakinin-I (NEB-SK-I).  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Sarcophagidae; Sarcophaga.  
OX NCBI\_TaxID=7385;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Head;  
RX MEDLINE=93083101; PubMed=1360367;  
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;  
RT "Isolation and primary structure of two sulfakinin-like peptides from  
RT the fleshfly, Neobellieria bullata.";  
RL Comp. Biochem. Physiol. 103C:135-142(1992).  
CC -!- FUNCTION: Myotropic peptide.  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; 1.  
KW Neuropeptide; Amidation; Sulfation.  
FT MOD\_RES 4 4 SULFATION (POTENTIAL).  
FT MOD\_RES 9 9 AMIDATION (POTENTIAL).  
SQ SEQUENCE 9 AA; 1187 MW; 8B0A0691B86B5AAA CRC64;

Query Match 25.5%; Score 13; DB 1; Length 9;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 YKNSKF 9  
| : |  
Db 4 YGHMRF 9

RESULT 44  
ESTA\_SCHGA STANDARD; PRT; 10 AA.  
ID P81012;  
AC P81012;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Esterase 52 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)  
DE (Fragment).  
OS Schizaphis graminum (Aphid).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
OC Aphidoidea; Aphididae; Aphidini; Schizaphis.  
OX NCBI\_TaxID=13262;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=97468499; PubMed=9327586;  
RA Siegfried B.D., Ono M., Swanson J.J.;  
RT "Purification and characterization of a carboxylesterase associated  
RT with organophosphate resistance in the greenbug, Schizaphis graminum  
RT (Homoptera: Aphididae).";  
RL Arch. Insect Biochem. Physiol. 36:229-240(1997).  
CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a  
CC carboxylic anion.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
DR InterPro; IPR002018; CarboxylesteraseB.  
DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; PARTIAL.  
DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; PARTIAL.  
KW Hydrolase; Serine esterase.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1025 MW; 018ABE587865A2C0 CRC64;

Query Match 25.5%; Score 13; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GY 4  
| : |  
Db 7 GY 8

RESULT 45  
HTF\_HELZE  
ID HTF\_HELZE STANDARD; PRT; 10 AA.  
AC P16353;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypertrehalosaemic hormone (He2-HRTH).  
OS Heliothis zea (Corn earworm) (Bollworm).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Noctuidae; Heliothinae; Helicoverpa.  
OX NCBI\_TaxID=7113;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Corpora cardiaca;  
RX MEDLINE=88326324; PubMed=3415690;  
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,  
RA Tseng C.M., Zhang Y.S., Hayes D.K.;  
RT "Isolation and primary structure of a neuropeptide hormone from  
RT Heliothis zea with hypertrehalosemic and adipokinetic activities.";  
RL Biochem. Biophys. Res. Commun. 155:344-350(1988).  
CC -1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that  
CC elevate the level of trehalose in the hemolymph (trehalose is the  
CC major carbohydrate in the hemolymph of insects).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.  
DR PIR; A31571; A31571.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;

Query Match 25.5%; Score 13; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.1e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3  
| : |  
Db 7 GWG 9

Search completed: August 30, 2004, 10:50:20  
Job time : 3.55068 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 2.70608 Seconds  
(without alignments)  
319.918 Million cell updates/sec

Title: US-09-720-469A-3  
Perfect score: 51  
Sequence: 1 GFGYKNSKF 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 23    | 45.1        | 13     | 2 PT0331 | Ig heavy chain CRD |
| 2          | 23    | 45.1        | 14     | 2 S36678 | dodecenoyl-CoA Del |
| 3          | 22    | 43.1        | 12     | 2 PH1454 | T-cell receptor al |
| 4          | 22    | 43.1        | 13     | 2 PH0787 | T-cell receptor al |
| 5          | 21    | 41.2        | 8      | 2 PC4373 | telomeric and tetr |
| 6          | 20    | 39.2        | 9      | 2 UP0073 | ribosomal protein  |
| 7          | 20    | 39.2        | 10     | 2 B33995 | hypotrehalosemic h |
| 8          | 20    | 39.2        | 11     | 2 PT0211 | T-cell receptor al |
| 9          | 20    | 39.2        | 11     | 2 S38307 | DEB-A protein - fr |
| 10         | 19    | 37.3        | 10     | 2 B61033 | ranatachykinin B - |
| 11         | 19    | 37.3        | 14     | 2 B58502 | 36K kidney stone p |
| 12         | 18    | 35.3        | 9      | 2 PC7074 | translation elonga |
| 13         | 18    | 35.3        | 10     | 2 F60527 | sperm-activating p |
| 14         | 18    | 35.3        | 10     | 2 B60589 | hypothetical prote |
| 15         | 18    | 35.3        | 10     | 2 S06964 | beta-fructofurans  |
| 16         | 18    | 35.3        | 10     | 2 PQ0753 | 20alpha-hydroxyste |
| 17         | 18    | 35.3        | 11     | 2 A44755 | T-cell receptor be |
| 18         | 18    | 35.3        | 12     | 2 S26547 | Ig heavy chain CRD |
| 19         | 18    | 35.3        | 12     | 2 PT0274 | VCAM-1 5'UTR bindi |
| 20         | 18    | 35.3        | 13     | 2 A59387 | glyceraldhyde-3-P  |
| 21         | 18    | 35.3        | 13     | 2 PS0277 | histone H4-1 precu |
| 22         | 18    | 35.3        | 14     | 2 I51432 | glucose 1-dehydrog |
| 23         | 18    | 35.3        | 14     | 2 A17150 | acetyl ornithine d |
| 24         | 17    | 33.3        | 11     | 2 I41138 | spermadhesin AQN-3 |
| 25         | 17    | 33.3        | 11     | 2 S68649 | T-cell receptor be |
| 26         | 17    | 33.3        | 11     | 2 PH0939 | bradykinin-like pe |
| 27         | 17    | 33.3        | 13     | 2 A61361 | Ig H chain V-D-J r |
| 28         | 17    | 33.3        | 14     | 2 PH1597 | unidentified 27.2K |
| 29         | 17    | 33.3        | 14     | 2 PC7079 |                    |

|    |    |      |    |          |                    |
|----|----|------|----|----------|--------------------|
| 30 | 17 | 33.3 | 14 | 2 C59137 | protein pf3 - gold |
| 31 | 16 | 31.4 | 9  | 2 A42266 | peptidylglycine mo |
| 32 | 16 | 31.4 | 10 | 2 C45474 | thrombospondin 2 - |
| 33 | 16 | 31.4 | 10 | 2 PT0243 | Ig heavy chain CRD |
| 34 | 16 | 31.4 | 12 | 1 UTU60  | tremmerogen A-10 - |
| 35 | 16 | 31.4 | 12 | 2 S26548 | T-cell receptor be |
| 36 | 16 | 31.4 | 12 | 2 S47391 | T-cell antigen rec |
| 37 | 16 | 31.4 | 12 | 2 S47395 | T-cell antigen rec |
| 38 | 16 | 31.4 | 12 | 2 S63492 | dissimilatory sulf |
| 39 | 16 | 31.4 | 13 | 2 PT0263 | Ig heavy chain CRD |
| 40 | 16 | 31.4 | 13 | 2 PT0304 | Ig heavy chain CRD |
| 41 | 16 | 31.4 | 14 | 2 I51430 | hemoglobin beta ch |
| 42 | 16 | 31.4 | 14 | 2 PH1586 | Ig H chain V-D-J r |
| 43 | 16 | 31.4 | 14 | 2 S37141 | rpsA protein - Erw |
| 44 | 15 | 29.4 | 8  | 2 PH1618 | Ig H chain V-D-J r |
| 45 | 15 | 29.4 | 8  | 2 PH1618 |                    |

ALIGNMENTS

RESULT 1  
PT0331  
Ig heavy chain CRD3 region (clone J2-121) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0331  
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.U.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A/Reference number: PT0222; MUID:91108337; PMID:1899102  
A/Accession: PT0331  
A/Molecule type: DNA  
A/Residues: 1-13 <YAM>  
A/Experimental source: B lymphocyte  
C/Keywords: heterotetramer; immunoglobulin

Query Match 45.1%; Score 23; DB 2; Length 13;  
Best Local Similarity 57.1%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GYKNSKF 9  
DB 6 GYNNPPF 12

RESULT 2  
S36678  
dodecenoyl-CoA Delta-isomerase (EC 5.3.3.8) / enoyl-CoA hydratase (EC 4.2.1.17) / 3-hydr  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Mar-1997 #sequence\_revision 07-Nov-1997 #text\_change 24-Jul-1998  
C/Accession: S36678  
R/Chen, N.; Crane, D.I.  
Biochem. J. 283, 605-610, 1992  
A/Title: Induction of the major integral membrane protein of mouse liver peroxisomes by  
A/Reference number: S21285; MUID:92246895; PMID:1575703  
A/Accession: S36678  
A/Molecule type: protein  
A/Residues: 1-14 <CHE>  
A/Experimental source: liver  
C/Function:  
A/Pathway: fatty acid beta-oxidation  
C/Keywords: carbon-oxygen lyase; fatty acid beta-oxidation; hydro-lyase; intramolecular

Query Match 45.1%; Score 23; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGKNSKF 9  
DB 1 FGFKMGPF 8

## RESULT 3

PH1454  
T-cell receptor alpha chain (clone A3/72.2) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
C/Accession: PH1454  
R/Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kd  
J. Exp. Med. 177, 811-820, 1993  
A/Title: T cell receptor selection by and recognition of two class I major histocompatib  
A/Reference number: PH1430; MUID:93171821; PMID:8436911  
C/Accession: PH1454  
A/Molecule type: mRNA  
A/Residues: 1-12 <CAS>  
A/Experimental source: cytolitic T-lymphocyte  
C/Superfamily: immunoglobulin homology  
C/Keywords: receptor; T-cell

Query Match 43.1%; Score 22; DB 2; Length 12;  
Best Local Similarity 57.1%; Pred. No. 5.6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GYKNSKF 9  
||:|  
Db 5 GYQNFYF 11

## RESULT 4

PH0787  
T-cell receptor alpha chain (F8) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C/Accession: PH0787  
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-T  
allelic exclusion and antigen-specific repertoire.  
A/Reference number: PH0746; MUID:92078846; PMID:1836010  
C/Accession: PH0787  
A/Molecule type: mRNA  
A/Residues: 1-13 <CAS>  
A/Cross-references: EMBL:X60891  
A/Experimental source: T lymphocyte  
C/Keywords: T-cell receptor

Query Match 43.1%; Score 22; DB 2; Length 13;  
Best Local Similarity 57.1%; Pred. No. 6.1e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GYKNSKF 9  
||:|  
Db 6 GYQNFYF 12

## RESULT 5

PC4373  
telomeric and tetraplex DNA binding protein qTBP42 III - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 28-Oct-1997 #sequence\_revision 28-Oct-1997 #text\_change 07-May-1999  
C/Accession: PC4373  
R/Sarig, G.; Weisman-Shomer, P.; Fry, M.  
Biochem. Biophys. Res. Commun. 237, 617-623, 1997  
A/Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA  
A/Reference number: PC4371; MUID:97445086; PMID:9299414  
C/Accession: PC4373  
A/Molecule type: protein  
A/Residues: 1-8 <SAR>  
C/Comment: This protein binds either strand of the telomeric DNA as well as unimolecular  
F,1-4/Domain: RNPI #status predicted <RNP>

Query Match 41.2%; Score 21; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFQY 4  
||:|  
Db 1 GFQF 4

## RESULT 6

JP0073  
ribosomal protein L32 - Leuconostoc mesenteroides (fragment)  
C/Species: Leuconostoc mesenteroides  
C/Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 28-Oct-1994  
C/Accession: JP0073  
R/Ochi, K.  
submitted to JIPID, February 1994  
A/Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pro  
A/Reference number: JP0042  
C/Accession: JP0073  
A/Molecule type: protein  
A/Residues: 1-9 <OCH>  
C/Keywords: protein biosynthesis; ribosome

Query Match 39.2%; Score 20; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KNSK 8  
|||  
Db 6 KNSK 9

## RESULT 7

B33995  
hypotrehalosemic hormone - black horse fly  
C/Species: Tabanus atratus (black horse fly)  
C/Date: 23-Mar-1990 #sequence\_revision 23-Mar-1990 #text\_change 31-Oct-1997  
C/Accession: B33995  
R/Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Y  
Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989  
A/Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehaloc  
A/Reference number: A33995; MUID:90046758; PMID:2813385  
C/Accession: B33995  
A/Molecule type: protein  
A/Residues: 1-10 <UAF>  
C/Superfamily: adipokinetic hormone  
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F,1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted  
F,10/Modified site: amidated carboxyl end (Tyr) #status predicted

Query Match 39.2%; Score 20; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFQY 4  
||:|  
Db 7 GFQY 10

## RESULT 8

PT0211  
T-cell receptor alpha chain V-J region (4-1-G.4) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997  
C/Accession: PT0211  
R/Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.  
J. Exp. Med. 173, 1091-1097, 1991  
A/Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict  
A/Reference number: PT0209; MUID:91217621; PMID:1902501  
C/Accession: PT0211  
A/Molecule type: mRNA  
A/Residues: 1-11 <NAK>  
C/Keywords: T-cell receptor

Query Match 39.2%; Score 20; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.2e+03;



Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GYKN 6  
||:|  
Db 8 GYQN 11

## RESULT 9

S38307  
DEB-A protein - fruit fly (Drosophila melanogaster) (fragment)  
C/Species: Drosophila melanogaster  
C/Date: 19-May-1994 #sequence\_revision 27-Feb-1997 #text\_change 17-Mar-1999  
C/Accession: S38307  
R/Wang, G.L.; Goldstein, E.S.  
Biochim. Biophys. Acta 1216, 94-104, 1993  
A/Title: An AP-1 binding site in the upstream region of DEB-A is part of a developmental  
A/Reference number: S38307; MUID:94032494; PMID:8218421  
A/Accession: S38307  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-14 <WAN>

Query Match 39.2%; Score 20; DB 2; Length 14;  
Best Local Similarity 66.7%; Pred. No. 1.6e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 FGYN 7  
||| |  
Db 4 FGYS 9

## RESULT 10

B61033  
ranatachykinin B - bullfrog  
C/Species: Rana catesbeiana (bullfrog)  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Aug-2000  
C/Accession: B61033; JE0427  
R/Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.  
Regul. Pept. 42(Suppl.1), S12, 1992  
A/Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and inte  
A/Reference number: A61033  
A/Accession: B61033  
A/Molecule type: protein  
A/Residues: 1-10 <KAN>  
R/Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.  
Biochem. Biophys. Res. Commun. 177, 588-595, 1991  
A/Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and inte  
A/Reference number: JE0426; MUID:91254337; PMID:2043143  
A/Accession: JE0427  
A/Molecule type: protein  
A/Residues: 1-10 <KOZ>  
C/Superfamily: unassigned animal peptides  
C/Keywords: amidated carboxyl end; neuropeptide  
F/10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.3%; Score 19; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 4 YKNSKF 9  
||:|  
Db 1 YKSDSF 6

## RESULT 11

B58502  
36K kidney stone protein - unidentified bacterium (fragment)  
C/Species: unidentified bacterium  
C/Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
C/Accession: B58502  
R/Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A/Description: The proteins of kidney and gallbladder stones.

A/Reference number: A58501  
A/Accession: B58502  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-14 <BIN>  
A/Experimental source: human kidney stone containing Ca ox.monox dihyd, 1% struvite, CaPc  
A/Note: tentative identification of 8-Tyr and 9-Thr

Query Match 37.3%; Score 19; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 FG Y 4  
||| |  
Db 6 FG Y 8

## RESULT 12

PC7074  
translation elongation factor eEF-1 beta chain - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C/Accession: PC7074  
R/Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.; I  
Electrophoresis 21, 1853-1871, 2000  
A/Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of t  
A/Reference number: PC7072  
A/Accession: PC7074  
A/Molecule type: protein  
A/Residues: 1-9 <TSU>  
A/Experimental source: strain C57BL/6C<sub>x</sub> Slc, male; brain, cortex  
C/Keywords: brain; cerebral cortex

Query Match 35.3%; Score 18; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GFG 3  
||| |  
Db 1 GFG 3

## RESULT 13

F60527  
sperm-activating peptide (Gly-3,5 SAP-I) - sea urchin (Tripneustes gratilla)  
N/Alternate names: speract homolog TG-8  
C/Species: Tripneustes gratilla  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
C/Accession: F60527; H39572  
R/Yoshino, K.I.; Kajitani, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguc  
Comp. Biochem. Physiol. B 94, 739-751, 1989  
A/Title: A halogenated amino acid-containing sperm activating peptide and its related pe  
otus nudus, Echinometra mathaei and Heterocentrotus mamillatus.  
A/Reference number: A60527  
A/Accession: F60527  
A/Molecule type: protein  
A/Residues: 1-10 <YOS>  
A/Note: this peptide did not contain bromophenylalanine  
R/Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; St  
Biochemistry 30, 6203-6209, 1991  
A/Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associate  
A/Reference number: A39572; MUID:91283461; PMID:2059627  
A/Accession: H39572  
A/Molecule type: protein  
A/Residues: 1-10 <YOS>  
A/Note: this peptide contained bromophenylalanine  
C/Superfamily: unassigned animal peptides  
C/Keywords: bromine  
F/2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match 35.3%; Score 18; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3  
|||  
Db 1 GFG 3

## RESULT 14

B60589

sperm-activating peptide (Gly-3, Ser-5, Ile-9 SAP-I) - slate-pencil urchin (Heterocentroc  
C/Species: Heterocentrocetus mammillatus  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
C/Accession: B60589  
R/Yoshino, K.I.; Kajiyura, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguchi,  
Comp. Biochem. Physiol. B 94, 739-751, 1989  
A/Title: A halogenated amino acid-containing sperm activating peptide and its related pe  
otus nudus, Echinopecten mathaei and Heterocentrocetus mammillatus.  
A/Reference number: A60527  
A/Accession: B60589  
A/Molecule type: protein  
A/Residues: 1-10 <YOS>  
C/Superfamily: unassigned animal peptides

Query Match 35.3%; Score 18; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3  
|||  
Db 1 GFG 3

## RESULT 15

S06964

hypothetical protein (nifa 5' region) - Rhizobium leguminosarum (fragment)  
C/Species: Rhizobium leguminosarum  
C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 08-Oct-1999  
C/Accession: S06964  
R/Roelvink, P.W.; Hontelez, J.G.J.; van Kammen, A.; van den Bos, R.C.  
Mol. Microbiol. 3, 1441-1447, 1989  
A/Title: Nucleotide sequence of the regulatory nifa gene of Rhizobium leguminosarum PRF:  
A/Reference number: S06964; MUID:90136072; PMID:2693897  
A/Accession: S06964  
A/Molecule type: DNA  
A/Residues: 1-10 <ROE>  
A/Cross-references: EMBL:X17073; NID:G46208; PIDN:CAA34923.1; PID:G809748

Query Match 35.3%; Score 18; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3  
|||  
Db 3 GFG 5

## RESULT 16

PQ0753

beta-fructofuranosidase (EC 3.2.1.26) IIB - barley (fragment)  
C/Species: Hordeum vulgare (barley)  
C/Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 23-Mar-1995  
C/Accession: PQ0753  
R/Oberland, D.M.; Simmen, U.; Bolter, T.; Wienken, A.  
Plant Physiol. 101, 1331-1339, 1993  
A/Title: Purification and characterization of three soluble invertases from barley (Hord  
A/Reference number: PQ0752; MUID:94143483; PMID:8310063  
A/Accession: PQ0753  
A/Molecule type: protein  
A/Residues: 1-10 <OBE>  
A/Experimental source: leaf, cv. Express  
C/Keywords: alternative initiators; glycoprotein; glycosidase; hydrolase

Query Match 35.3%; Score 18; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 2.7e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GFGYKNS 7  
|||:  
Db 1 GFGPDNT 7

## RESULT 17

A44755

20alpha-hydroxysteroid dehydrogenase (EC 1.1.1.149) - Clostridium scindens (fragment)  
C/Species: Clostridium scindens  
C/Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 17-Mar-1999  
C/Accession: A44755  
R/Krafft, A.E.; Hylemon, P.B.  
J. Bacteriol. 171, 2925-2932, 1989  
A/Title: Purification and characterization of a novel form of 20alpha-hydroxysteroid dehy  
A/Reference number: A44755; MUID:89255043; PMID:2722736  
A/Accession: A44755  
A/Molecule type: protein  
A/Residues: 1-11 <KRA>  
C/Comment: This enzyme was purified to homogeneity and shown to have 20alpha hydroxyster  
sphate dehydrogenase (GAPDH) activity although the fragment shows near identity to known  
C/Keywords: homotetramer; NAD; NADP; oxidoreductase

Query Match 35.3%; Score 18; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3  
|||  
Db 8 GFG 10

## RESULT 18

S26547

T-cell receptor beta chain (clone Cw3/10.1) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
C/Accession: S26547  
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Widm  
J. Exp. Med. 176, 439-447, 1992  
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A/Reference number: S26512; MUID:92364546; PMID:1380061  
A/Accession: S26547  
A/Molecule type: mRNA  
A/Residues: 1-12 <CAS>  
A/Cross-references: EMBL:X67997  
A/Experimental source: cytolytic T-lymphocyte, clone Cw3/10.1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: T-cell receptor

Query Match 35.3%; Score 18; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4  
|||  
Db 6 GFGY 9

## RESULT 19

PT0274

Ig heavy chain CRD3 region (clone 3-109B) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0274  
R/Yamada, M.; Wasserman, R.; Reichardt, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j  
A/Reference number: PT0222; MUID:91108337; PMID:1899102  
A/Accession: PT0274  
A/Molecule type: DNA  
A/Residues: 1-12 <YAM>

A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 35.3%; Score 18; DB 2; Length 12;  
Best Local Similarity 60.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKNS 7  
|||  
Db 2 GYSSS 6

RESULT 20  
A59387  
VCAM-1 5'UTR binding protein - Rana pipiens (fragment)

C;Species: Rana pipiens  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
C;Accession: A59387  
R;BANNERJEE, H.  
submitted to the Protein Sequence Database, February 2001  
A;Description: Identification and characterization of a novel VCAM-1 5'UTR.  
A;Reference number: A59387

A;Accession: A59387  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-13 <BAN>  
A;Experimental source: CCL-145  
A;Note: VCAM-1 5' untranslated region binding protein with a probable translation inhibi

Query Match 35.3%; Score 18; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYK 5  
|||  
Db 8 GYK 10

RESULT 21

PS0277  
glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - rice (strain  
C;Species: Oryza sativa (rice)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 03-Jun-2002  
C;Accession: PS0277  
R;Tsugita, A.  
submitted to JIPID, April 1993

A;Reference number: PS0206  
A;Accession: PS0277  
A;Molecule type: protein  
A;Residues: 1-13 <TSU>  
A;Experimental source: leaf, chlorophyll, stem  
C;Keywords: oxidoreductase

Query Match 35.3%; Score 18; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3  
|||  
Db 9 GFG 11

RESULT 22

151432  
histone H4-1 precursor - African clawed frog (fragment)  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 23-Jul-1999  
C;Accession: 151432  
R;Gargiulo, G.; Razvi, F.; Ruberti, I.; Mohr, I.; Worcel, A.  
J. Mol. Biol. 181, 333-349, 1985  
A;Title: Chromatin-specific hypersensitive sites are assembled on a Xenopus histone gene  
A;Reference number: 151431; MUID:85160855; PMID:4039007  
A;Accession: 151432

A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-14 <GAR>  
A;Cross-references: GB:M23777; NID:G214219; PIDN:AAA49737.1; PID:G214222  
C;Superfamily: histone H4

Query Match 35.3%; Score 18; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3  
|||  
Db 11 GFG 13

RESULT 23

A17150  
glucose 1-dehydrogenase (NAD) (EC 1.1.1.118) - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 03-Jun-2002  
C;Accession: A17150  
R;Franzen, B.; Carrubba, C.; Feingold, D.S.; Ashcom, J.; Franzen, J.S.  
Biochem. J. 199, 599-602, 1981  
A;Title: Amino acid sequence of the tryptic peptide containing the catalytic-site thiol  
A;Reference number: A17150; MUID:82182061; PMID:6896145  
A;Accession: A17150  
A;Molecule type: protein  
A;Residues: 1-14 <FRA>  
A;Keywords: NAD; oxidoreductase

Query Match 35.3%; Score 18; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3  
|||  
Db 4 GFG 6

RESULT 24

I41138  
acetyl ornithine deacetylase (argE) - Escherichia coli (fragment)  
C;Species: Escherichia coli  
C;Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 08-Oct-1999  
C;Accession: I41138  
R;Charlier, D.; Piette, J.; Glansdorff, N.  
Nucleic Acids Res. 10, 5935-5948, 1982  
A;Title: Is3 can function as a mobile promoter in E.coli.  
A;Reference number: I41137; MUID:83064529; PMID:6292860  
A;Accession: I41138  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-11 <RES>  
A;Cross-references: GB:J01589; NID:G145346; PIDN:AAA23485.1; PID:G551788

Query Match 33.3%; Score 17; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4  
|||  
Db 8 GFGY 11

RESULT 25

S68649  
spermadhesin AQN-3 - pig (fragments)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 17-Mar-1999  
C;Accession: S68649  
R;Calvete, J.J.; Dostalova, Z.; Sanz, L.; Adertmann, K.; Thole, H.H.; Toepfer-Petersen, E.  
FEBS Lett. 379, 207-211, 1996  
A;Title: Mapping the heparin-binding domain of boar spermadhesins.

A:Reference number: S68648; MUID:96184566; PMID:8603690  
A:Accession: S68649  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-6;7-11 <CAL>

Query Match 33.3%; Score 17; DB 2; Length 11;  
Best Local Similarity 42.9%; Pred. No. 4.5e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKMS 7  
| | | |  
| | | |  
Db 5 GMYQSS 11

#### RESULT 26

PH0939  
T-cell receptor beta chain V-D-J region (clone 10) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0939  
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy  
A:Reference number: PH0891; MUID:92078857; PMID:1836012  
A:Accession: PH0939  
A:Molecule type: mRNA  
A:Residues: 1-11 <GOL>  
A:Experimental source: complete Freund's adjuvant-immunized lymph node  
C:Keywords: T-cell receptor

Query Match 33.3%; Score 17; DB 2; Length 11;  
Best Local Similarity 60.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKMS 7  
| | | |  
| | | |  
Db 7 GLKNT 11

#### RESULT 27

A61361  
bradykinin-like peptide - Bombina orientalis  
C:Species: Bombina orientalis  
C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 18-Aug-2000  
C:Accession: A61361  
R:Yasuhara, T.; Hira, M.; Nakajima, T.; Yanaihara, N.; Yanaihara, C.; Hashimoto, T.; Sak  
Chem. Pharm. Bull. 21, 1388-1391, 1973  
A:Title: Active peptides on smooth muscle in the skin of Bombina orientalis Boulenger an  
A:Reference number: A61361; MUID:73256822; PMID:4732297  
A:Accession: A61361  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <YAS>  
C:Superfamily: unassigned animal peptides  
C:Keywords: skin

Query Match 33.3%; Score 17; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 5.3e+03;  
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GFGYKNSKF 9  
| | | |  
| | | |  
Db 4 GFSPFRGKF 12

#### RESULT 28

PH1597  
Ig H chain V-D-J region (wild-type clone 304) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1597  
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993  
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A:Reference number: PH1580; MUID:93301609; PMID:8315367  
A:Accession: PH1597  
A:Molecule type: DNA  
A:Residues: 1-14 <LEV>  
A:Experimental source: bone marrow pre-B lymphocyte  
C:Keywords: immunoglobulin

Query Match 33.3%; Score 17; DB 2; Length 14;  
Best Local Similarity 75.0%; Pred. No. 5.7e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4  
| | | |  
| | | |  
Db 5 GSGY 8

#### RESULT 29

PC7079  
unidentified 27.2K protein - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C:Accession: PC7079  
R:Tsuigita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.; N  
Electrophoresis 21, 1853-1871, 2000  
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of tri  
A:Reference number: PC7072  
A:Accession: PC7079  
A:Molecule type: protein  
A:Residues: 1-14 <TSU>  
A:Experimental source: strain C57BL/6Cr Slc, male; brain, striatum  
C:Keywords: brain

Query Match 33.3%; Score 17; DB 2; Length 14;  
Best Local Similarity 42.9%; Pred. No. 5.7e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGYKNSK 8  
| | | |  
| | | |  
Db 2 YKYVKK 8

#### RESULT 30

C59137  
protein Pf3 - golden needle mushroom (fragment)  
C:Species: Flammulina velutipes (golden needle mushroom)  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: C59137  
R:Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.  
submitted to the Protein Sequence Database, November 1999  
A:Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr  
A:Reference number: A59137  
A:Accession: C59137  
A:Molecule type: protein  
A:Residues: 1-14 <SAK>

Query Match 33.3%; Score 17; DB 2; Length 14;  
Best Local Similarity 75.0%; Pred. No. 5.7e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4  
| | | |  
| | | |  
Db 5 GFKY 8

#### RESULT 31

A42266  
peptidylglycine monooxygenase (EC 1.14.17.3), rPAM-5 - rat (fragment)  
N:Alternate names: peptidylglycine alpha-amidating monooxygenase  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 26-May-1995  
C:Accession: A42266

R.Eipper, B.A.; Green, C.B.; Campbell, T.A.; Stoffers, D.A.; Keutmann, H.T.; Mains, R.E.  
J. Biol. Chem. 267, 4008-4015, 1992  
A>Title: Alternative splicing and endoproteolytic processing generate tissue-specific fo  
A/Reference number: A42266; MUID:92156145; PMID:1740449  
A/Accession: A42266  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-9 <EIP>  
A/Experimental source: pituitary  
A/Note: sequence extracted from NCBI backbone (NCBIN:82733, NCBI:82750)  
C/Keywords: oxidoreductase

Query Match 31.4%; Score 16; DB 2; Length 9;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 GYKNS 7  
| | | | |  
Db 4 GFKDT 8

RESULT 32  
C45474  
thrombospondin 2 - bovine (fragment)  
N/Alternate names: corticotropin-induced secreted protein (CISP); thrombospondin homolog  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 14-Aug-1998  
C/Accession: C45474  
R/Pellerin, S.; Lafeuillade, B.; Scherrer, N.; Gagnon, J.; Shi, D.L.; Chambaz, E.M.; Fei  
J. Biol. Chem. 268, 4304-4310, 1993  
A/Title: Corticotropin-induced secreted protein, an ACTH-induced protein secreted by adr  
A/Reference number: A45474; MUID:93179438; PMID:8382699  
A/Accession: C45474  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <PEL>  
A/Experimental source: adrenocortical cells  
A/Note: sequence extracted from NCBI backbone (NCBI:125844)  
C/Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; v

Query Match 31.4%; Score 16; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 6.3e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 FGy 4  
| | | | |  
Db 2 YGY 4

RESULT 33  
PT0243  
Ig heavy chain CRD3 region (clone 2-103A) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0243  
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A/Reference number: PT0222; MUID:91108337; PMID:1899102  
A/Accession: PT0243  
A/Molecule type: DNA  
A/Residues: 1-10 <YAM>  
A/Experimental source: B lymphocyte  
C/Keywords: heterotetramer; immunoglobulin

Query Match 31.4%; Score 16; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 6.3e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 GYKNS 7  
| | | | |  
Db 2 GYDYS 6

RESULT 34  
JTUGO  
tremmerogen A-10 - jelly fungus (Tremella mesenterica)  
C/Species: Tremella mesenterica  
C/Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 07-Nov-1997  
C/Accession: A01642; A61313  
R/Sakagami, Y.; Yoshida, M.; Isogai, A.; Suzuki, A.  
Science 212, 1525-1527, 1981  
A/Title: Peptide sex hormones inducing conjugation tube formation in compatible mating-c  
A/Reference number: A94256  
A/Accession: A01642

A/Molecule type: protein  
A/Residues: 1-12 <SAK1>  
A/Note: the farnesyl may instead be (2E,6E,10Z)-12-hydroxyfarnesyl  
R/Sakagami, Y.; Isogai, A.; Suzuki, A.; Tamura, S.; Tsuchiya, E.; Fukui, S.  
Agric. Biol. Chem. 42, 1301-1302, 1978  
A/Title: Amino acid sequence of tremmerogen A-10, a peptidal hormone, inducing conjugatio  
A/Reference number: A61313  
A/Accession: A61313  
A/Molecule type: protein  
A/Residues: 1-12 <SAK2>

C/Comment: Tremmerogen A-10 is produced by the A mating-type cells and induces formation  
C/Superfamily: tremmerogen a-13  
C/Keywords: extracellular protein; hormone; lipoprotein; methylated carboxyl end; pherom  
F/12/Binding site: farnesyl (Cys) (covalent) #status experimental  
F/12/Modified site: methyl ester carboxyl end (Cys) #status experimental

Query Match 31.4%; Score 16; DB 1; Length 12;  
Best Local Similarity 75.0%; Pred. No. 7.6e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GFgy 4  
| | | | |  
Db 8 GNGY 11

RESULT 35  
S26548  
T-cell receptor beta chain (clone Cw3/Cas3) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
C/Accession: S26548  
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
J. Exp. Med. 176, 439-447, 1992  
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A/Reference number: S26512; MUID:92364546; PMID:1380061  
A/Accession: S26548  
A/Molecule type: mRNA  
A/Residues: 1-12 <CAS>  
A/Cross-references: EMBL:X67998  
A/Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas3  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: T-cell receptor

Query Match 31.4%; Score 16; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 7.6e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GFgy 4  
| | | | |  
Db 6 GQGY 9

RESULT 36  
S47391  
T-cell antigen receptor VJ junction beta chain - human  
C/Species: Homo sapiens (man)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
C/Accession: S47391; S47386  
R/Lehner, P.J.  
submitted to the EMBL Data Library, August 1994  
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c

A;Reference number: S47355  
A;Accession: S47391  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-12 <LEH>  
A;Cross-references: EMBL:Z35712; NID:G527519; PIDN:CAA84781.1; PID:G527520; EMBL:Z35701;  
C;Keywords: T-cell receptor

Query Match 31.4%; Score 16; DB 2; Length 12;  
Best Local Similarity 66.7%; Pred. No. 7.6e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGY 4  
: ||  
Db 8 YGY 10

## RESULT 37

S47394  
T-cell antigen receptor VJ junction beta chain - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
C;Accession: S47394; S47369  
R;Lehner, P.J.  
Submitted to the EMBL Data Library, August 1994  
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T C  
A;Reference number: S47355  
A;Accession: S47394  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-12 <LEH>  
A;Cross-references: EMBL:Z35714; NID:G527523; PIDN:CAA84783.1; PID:G527524; EMBL:Z35694;  
C;Keywords: T-cell receptor

Query Match 31.4%; Score 16; DB 2; Length 12;  
Best Local Similarity 66.7%; Pred. No. 7.6e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGY 4  
: ||  
Db 8 YGY 10

## RESULT 38

S47395  
T-cell antigen receptor VJ junction beta chain - human  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
C;Accession: S47395  
R;Lehner, P.J.  
Submitted to the EMBL Data Library, August 1994  
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T C  
A;Reference number: S47355  
A;Accession: S47395  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-12 <LEH>  
A;Cross-references: EMBL:Z35715; NID:G527525; PIDN:CAA84784.1; PID:G527526  
C;Keywords: T-cell receptor

Query Match 31.4%; Score 16; DB 2; Length 12;  
Best Local Similarity 66.7%; Pred. No. 7.6e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGY 4  
: ||  
Db 8 YGY 10

## RESULT 39

S63492  
dissimilatory sulfite reductase beta chain, soluble - Desulfovibrio desulfuricans (fragm  
C;Species: Desulfovibrio desulfuricans

C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
C;Accession: S63492  
R;Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kromeck, P.M.H.  
Eur. J. Biochem. 233, 873-879, 1995  
A;Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio c  
A;Reference number: S63489; MUID:96085152; PMID:8521853  
A;Accession: S63492  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-13 <STE>

Query Match 31.4%; Score 16; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 8.2e+03;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GYKSK 8  
|||  
Db 6 GYNPK 11

## RESULT 40

PT0263  
Ig heavy chain CRD3 region (clone 2-121B) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0263  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j c  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0263  
A;Molecule type: DNA  
A;Residues: 1-13 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 31.4%; Score 16; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 8.2e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4  
|||  
Db 2 GGGY 5

## RESULT 41

PT0304  
Ig heavy chain CRD3 region (clone 5-115B) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0304  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j c  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0304  
A;Molecule type: DNA  
A;Residues: 1-13 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 31.4%; Score 16; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 8.2e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGY 4  
: ||  
Db 2 YGY 4

## RESULT 42

I51430  
hemoglobin beta chain - African clawed frog (fragment)



C;Species: Xenopus laevis (African clawed frog)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 19-May-2000  
C;Accession: I51430  
R;Kay, R.M.; Harris, R.; Patient, R.K.; Williams, J.G.  
Nucleic Acids Res. 8, 2691-2707, 1980  
A;Title: Molecular cloning of cDNA sequences coding for the major alpha- and beta-globin  
A;Reference number: I51428; MUID:81053706; PMID:7001356  
A;Accession: I51430  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-14 <KAY>  
A;Cross-references: GB:M10601, NID:G214211, PIDN:AAA49735.1, PID:G214212  
C;Superfamily: globin; globin homology  
C;Keywords: blood; oxygen carrier

Query Match 31.4%; Score 16; DB 2; Length 14;  
Best Local Similarity 75.0%; Pred. No. 8.8e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4  
|:|  
Db 10 GKGY 13

## RESULT 43

PH1586  
Ig H chain V-D-J region (wild-type clone 10) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C;Accession: PH1586  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A;Reference number: PH1580; MUID:93301609; PMID:8315387  
A;Accession: PH1586  
A;Molecule type: DNA  
A;Residues: 1-14 <LEV>  
A;Experimental source: bone marrow pre-B lymphocyte  
C;Keywords: immunoglobulin

Query Match 31.4%; Score 16; DB 2; Length 14;  
Best Local Similarity 66.7%; Pred. No. 8.8e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGY 4  
|:|  
Db 8 YGY 10

## RESULT 44

S37141  
rpsA protein - Erwinia chrysanthemi  
C;Species: Erwinia chrysanthemi  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Oct-1999  
C;Accession: S37141  
R;Doutillie, A.; Toussaint, A.; Faelen, M.  
submitted to the EMBL Data Library, August 1993  
A;Description: Identification of the integration host factor genes of E. chrysanthemi.  
A;Reference number: S37139  
A;Accession: S37141  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-8 <DOU>  
A;Cross-references: EMBL:X74750; NID:G399669; PIDN:CAA52769.1; PID:G581108

Query Match 29.4%; Score 15; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 YKNSK 8  
|:|:|  
Db 2 FKSAK 6

## RESULT 45

PH1618  
Ig H chain V-D-J region (clone B-less 33) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C;Accession: PH1618  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A;Reference number: PH1580; MUID:93301609; PMID:8315387  
A;Accession: PH1618  
A;Molecule type: DNA  
A;Residues: 1-8 <LEV>  
A;Experimental source: bone marrow pre-B lymphocyte  
C;Keywords: immunoglobulin

Query Match 29.4%; Score 15; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3  
|:|  
Db 5 GYG 7

Search completed: August 30, 2004, 10:58:48  
Job time : 3.70608 secs



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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 11.0068 Seconds  
(without alignments)  
257.253 Million cell updates/sec

Title: US-09-720-469A-3  
Perfect score: 51  
Sequence: 1 GFGYKNSKF 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 149443

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                 | Description       |
|------------|-------|-------------|--------|--------------------|-------------------|
| 1          | 30    | 58.8        | 14     | US-10-421-503-13   | Sequence 13, Appl |
| 2          | 27    | 52.9        | 12     | US-09-226-666-4    | Sequence 4, Appl1 |
| 3          | 26    | 51.0        | 14     | US-10-239-313A-642 | Sequence 642, App |
| 4          | 25    | 49.0        | 9      | US-10-239-313A-542 | Sequence 542, App |
| 5          | 25    | 49.0        | 9      | US-10-239-313A-680 | Sequence 680, App |
| 6          | 25    | 49.0        | 10     | US-08-996-140-15   | Sequence 15, Appl |
| 7          | 25    | 49.0        | 12     | US-09-876-904A-78  | Sequence 78, Appl |
| 8          | 25    | 49.0        | 12     | US-10-226-795-15   | Sequence 15, Appl |
| 9          | 25    | 49.0        | 13     | US-09-205-658-263  | Sequence 263, App |
| 10         | 25    | 49.0        | 13     | US-09-963-693-263  | Sequence 263, App |
| 11         | 25    | 49.0        | 14     | US-09-791-378-526  | Sequence 526, App |
| 12         | 25    | 49.0        | 14     | US-09-826-290-313  | Sequence 313, App |
| 13         | 25    | 49.0        | 14     | US-10-449-829A-28  | Sequence 28, Appl |
| 14         | 25    | 49.0        | 14     | US-09-988-493-274  | Sequence 274, App |
| 15         | 25    | 49.0        | 14     | US-10-014-340-467  | Sequence 467, App |

|  | 16                | 17                | 18                | 19                | 20                | 21                   | 22                   | 23                | 24                | 25                | 26                | 27                | 28                | 29                | 30                 | 31                | 32                | 33                | 34                | 35                | 36                | 37                 | 38                | 39                | 40                | 41                 | 42                | 43                | 44                | 45                |
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|  | 25                | 25                | 25                | 25                | 24                | 24                   | 24                   | 24                | 24                | 24                | 24                | 24                | 24                | 24                | 24                 | 23                | 23                | 23                | 23                | 23                | 23                | 23                 | 23                | 23                | 23                | 23                 | 23                | 22                | 22                | 22                |
|  | 49.0              | 49.0              | 49.0              | 49.0              | 47.1              | 47.1                 | 47.1                 | 47.1              | 47.1              | 47.1              | 47.1              | 47.1              | 47.1              | 47.1              | 45.1               | 45.1              | 45.1              | 45.1              | 45.1              | 45.1              | 45.1              | 45.1               | 45.1              | 45.1              | 45.1              | 45.1               | 43.1              | 43.1              | 43.1              |                   |
|  | 14                | 14                | 14                | 14                | 9                 | 9                    | 9                    | 9                 | 9                 | 9                 | 9                 | 9                 | 9                 | 9                 | 8                  | 15                | 9                 | 9                 | 9                 | 9                 | 9                 | 10                 | 10                | 12                | 12                | 12                 | 12                | 9                 | 10                | 10                |
|  | US-10-014-340-468 | US-09-791-377-526 | US-10-255-679-60  | US-10-264-309-240 | US-09-780-053-158 | US-10-057-475B-10940 | US-10-154-884B-10940 | US-09-780-053-180 | US-09-780-053-304 | US-09-780-053-399 | US-09-780-053-472 | US-10-319-340-8   | US-10-013-815-35  | US-10-014-815-38  | US-10-014-485A-116 | US-10-387-486-10  | US-09-879-957-63  | US-10-460-512-6   | US-10-460-512-28  | US-10-003-983B-11 | US-10-807-856-63  | US-09-572-270A-623 | US-10-317-550-2   | US-10-302-100B-28 | US-10-474-601-12  | US-10-174-105A-153 | US-10-351-641-919 | US-09-799-250-154 | US-09-799-250-235 | US-09-799-250-330 |
|  | Sequence 468, App | Sequence 526, App | Sequence 60, Appl | Sequence 240, App | Sequence 158, App | Sequence 10940, A    | Sequence 10940, A    | Sequence 180, App | Sequence 304, App | Sequence 399, App | Sequence 472, App | Sequence 8, Appl1 | Sequence 35, Appl | Sequence 38, Appl | Sequence 116, App  | Sequence 10, Appl | Sequence 63, Appl | Sequence 6, Appl1 | Sequence 28, Appl | Sequence 11, Appl | Sequence 63, Appl | Sequence 623, App  | Sequence 2, Appl1 | Sequence 12, Appl | Sequence 153, App | Sequence 919, App  | Sequence 154, App | Sequence 235, App | Sequence 330, App |                   |

## ALIGNMENTS

RESULT 1  
US-10-421-503-13  
; Sequence 13, Application US/10421503  
; Publication No. US2004000922A1  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; TITLE OF INVENTION: Peptide inhibitors of protein kinase C  
; FILE REFERENCE: 58600-8210.US01  
; CURRENT APPLICATION NUMBER: US/10/421, 503  
; PRIOR FILING DATE: 2003-04-22  
; PRIOR APPLICATION NUMBER: US 60/374, 530  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: fragment derived from SEQ ID NO:6  
US-10-421-503-13

Query Match 58.8%; Score 30; DB 15; Length 14;  
Best Local Similarity 55.6%; Pred. No. 78;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GFGYKNSKF 9  
Db 2 GFGYTNPER 10

RESULT 2  
US-09-226-666-4  
; Sequence 4, Application US/09226666A  
; Patent No. US20020077282A1  
; GENERAL INFORMATION:  
; APPLICANT: Spacciapoli, Peter  
; APPLICANT: Rothstein, David M.

APPLICANT: Friden, Phillip M.  
TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS  
FILE REFERENCE: 50032/007001  
CURRENT APPLICATION NUMBER: US/09/226,666A  
CURRENT FILING DATE: 1999-01-08  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Derived from Homo sapiens  
US-09-226-666-4

Query Match 52.9%; Score 27; DB 9; Length 12;  
Best Local Similarity 62.5%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGYNKSKF 9  
Db 5 FGYNKSKF 12

RESULT 3  
US-10-239-313A-642  
Sequence 642, Application US/10239313A  
Publication No. US20030175285A1  
GENERAL INFORMATION:  
APPLICANT: KLINGUER - HAMOUR, Christine  
APPLICANT: CORVAIA, Nathalie  
APPLICANT: BECK, Alain  
APPLICANT: GOETSCH, Liliane  
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
FILE REFERENCE: 343 727 - US  
CURRENT APPLICATION NUMBER: US/10/239,313A  
CURRENT FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: FR 00/03711  
PRIOR FILING DATE: 2000-03-23  
PRIOR APPLICATION NUMBER: PCT 01/70772  
PRIOR FILING DATE: 2001-03-22  
NUMBER OF SEQ ID NOS: 697  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 642  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Clostridium tetani  
US-10-239-313A-642

Query Match 51.0%; Score 26; DB 14; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KNSKF 9  
Db 5 KNSKF 9

RESULT 4  
US-10-239-313A-542  
Sequence 542, Application US/10239313A  
Publication No. US20030175285A1  
GENERAL INFORMATION:  
APPLICANT: KLINGUER - HAMOUR, Christine  
APPLICANT: CORVAIA, Nathalie  
APPLICANT: BECK, Alain  
APPLICANT: GOETSCH, Liliane  
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
FILE REFERENCE: 343 727 - US

CURRENT APPLICATION NUMBER: US/10/239,313A  
CURRENT FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: FR 00/03711  
PRIOR FILING DATE: 2000-03-23  
PRIOR APPLICATION NUMBER: PCT 01/70772  
PRIOR FILING DATE: 2001-03-22  
NUMBER OF SEQ ID NOS: 697  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 542  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-239-313A-542

Query Match 49.0%; Score 25; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGY 4  
Db 4 GFGY 7

RESULT 5  
US-10-239-313A-680  
Sequence 680, Application US/10239313A  
Publication No. US20030175285A1  
GENERAL INFORMATION:  
APPLICANT: KLINGUER - HAMOUR, Christine  
APPLICANT: CORVAIA, Nathalie  
APPLICANT: BECK, Alain  
APPLICANT: GOETSCH, Liliane  
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
FILE REFERENCE: 343 727 - US  
CURRENT APPLICATION NUMBER: US/10/239,313A  
CURRENT FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: FR 00/03711  
PRIOR FILING DATE: 2000-03-23  
PRIOR APPLICATION NUMBER: PCT 01/70772  
PRIOR FILING DATE: 2001-03-22  
NUMBER OF SEQ ID NOS: 697  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 680  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-239-313A-680

Query Match 49.0%; Score 25; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGY 4  
Db 6 GFGY 9

RESULT 6  
US-08-996-140-15  
Sequence 15, Application US/08996140  
Publication No. US20030190318A1  
GENERAL INFORMATION:  
APPLICANT: TORIGOE, Kakuji  
APPLICANT: USHIO, Shimpel  
APPLICANT: KUNIKATA, Toshio  
APPLICANT: KURIMOTO, Masashi  
TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEWMARK  
STREET: 419 Seventh Street, N.W., Suite 300

```

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/996,140
  FILING DATE: 22-DEC-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: JP 356,426/1996
    FILING DATE: 26-DEC-1996
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: JP 52,526/1997
    FILING DATE: 21-FEB-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: JP 163,490/1997
    FILING DATE: 6-JUN-1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: JP 215,490/1997
    FILING DATE: 28-JUL-1997
  ATTORNEY/AGENT INFORMATION:
    NAME: BROWDY, Roger L.
    REGISTRATION NUMBER: 25,618
    REFERENCE/DOCKET NUMBER: TORIGOE=2
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 202-628-5197
      TELEFAX: 202-737-3528
  INFORMATION FOR SEQ ID NO: 15:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 10 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
    MOLECULE TYPE: peptide
    FRAGMENT TYPE: internal fragment
US-08-996-140-15

Query Match      49.0%; Score 25; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GFGY 4
      ||||
Db      7 GFGY 10

RESULT 7
US-09-876-904A-78
; Sequence 78, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOsome COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide crosslinked
US-09-876-904A-78

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Query Match          49.0%; Score 25; DB 10; Length 12;
Best Local Similarity 50.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKNSK 8
Db 2 GYGDNRKK 9

RESULT 8
US-10-226-795-15
; Sequence 15, Application US/10226795
; Publication No. US20040053865A1
; GENERAL INFORMATION:
; APPLICANT: HART, MARY KATE
; APPLICANT: WILSON, JULIE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
; TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN
; FILE REFERENCE: ARMY 166
; CURRENT APPLICATION NUMBER: US/10/226,795
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
; OTHER INFORMATION: chain of Mab EGP13C6-1-1 amino acid sequence
US-10-226-795-15

Query Match          49.0%; Score 25; DB 12; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGYKNS 7
Db 4 GGYDNA 9

RESULT 9
US-09-205-658-263
; Sequence 263, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogy, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 263
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-263

Query Match          49.0%; Score 25; DB 9; Length 13;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKN 6

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Db 2 GFGWTN 7

## RESULT 10

US-09-963-693-263  
; Sequence 263, Application US/09963693  
; Publication No. US20030181364A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruvkun, Gary  
; APPLICANT: Ogg, Scott  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR  
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS  
; FILE REFERENCE: 00786/351004  
; CURRENT APPLICATION NUMBER: US/09/963,693  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/09/205,658  
; PRIOR FILING DATE: 1998-12-03  
; PRIOR APPLICATION NUMBER: 08/857,076  
; PRIOR FILING DATE: 1997-05-15  
; PRIOR APPLICATION NUMBER: 08/888,534  
; PRIOR FILING DATE: 1997-07-07  
; PRIOR APPLICATION NUMBER: US98/10080  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 263  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-963-693-263

Query Match 49.0%; Score 25; DB 10; Length 13;  
Best Local Similarity 66.7%; Pred. No. 6e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKN 6  
Db 2 GFGWTN 7

## RESULT 11

US-09-791-378-526  
; Sequence 526, Application US/09791378  
; Patent No. US20020142303A1  
; GENERAL INFORMATION:  
; APPLICANT: Parekh, Rajesh  
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF  
; TITLE OF INVENTION: SCHIZOPHRENIA  
; FILE REFERENCE: 9195-061-999  
; CURRENT APPLICATION NUMBER: US/09/791,378  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 09/750,395  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 677  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 526  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-378-526

Query Match 49.0%; Score 25; DB 9; Length 14;  
Best Local Similarity 80.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYN 6  
Db 9 FGYSN 13

RESULT 12  
US-09-826-290-313

; Sequence 313, Application US/09826290  
; Patent No. US20020164668A1  
; GENERAL INFORMATION:  
; APPLICANT: Durham, L. Kathryn  
; APPLICANT: Friedman, David L.  
; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri  
; APPLICANT: Kimmel, Lida H.  
; APPLICANT: Parekh, Rajesh Bhikhu  
; APPLICANT: Potter, David M.  
; APPLICANT: Rohlf, Christian  
; APPLICANT: Silber, B. Michael  
; APPLICANT: Stieger, Thomas R.  
; APPLICANT: Sunderland, P. Trey  
; APPLICANT: Townsend, Robert Reid  
; APPLICANT: White, Frost  
; APPLICANT: Williams, Stephen A.

; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and  
; TITLE OF INVENTION: Uses Thereof, Including Diagnosis and Treatment of  
; TITLE OF INVENTION: Alzheimer's Disease  
; FILE REFERENCE: 2572-1-001 N2  
; CURRENT APPLICATION NUMBER: US/09/826,290  
; PRIOR FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/194,504  
; PRIOR FILING DATE: 2000-04-03  
; PRIOR APPLICATION NUMBER: US 60/253,647  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 492  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 313  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-09-826-290-313

Query Match 49.0%; Score 25; DB 9; Length 14;  
Best Local Similarity 80.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYN 6  
Db 9 FGYSN 13

## RESULT 13

US-10-449-829A-28  
; Sequence 28, Application US/10449829A  
; Publication No. US20040043425A1  
; GENERAL INFORMATION:  
; APPLICANT: Terrett, Jonathan Alexander  
; APPLICANT: Hall, Ian Phillip  
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF CHRON  
; TITLE OF INVENTION: ASTHMA  
; FILE REFERENCE: 2543-1-029  
; CURRENT APPLICATION NUMBER: US/10/449,829A  
; PRIOR FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: PCT/GB01/05476  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: P32060GB  
; PRIOR FILING DATE: 2000-12-08  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-449-829A-28

Query Match 49.0%; Score 25; DB 12; Length 14;  
Best Local Similarity 80.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYN 6  
Db 9 FGYSN 13



Db 9 FGYSN 13

## RESULT 14

US-09-988-493-274  
; Sequence 274, Application US/09988493  
; Publication No. US20030064419A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, Herath Mudiysanselage Achula Chandrasiri  
; APPLICANT: O'Hare, Michael John  
; APPLICANT: Page, Martin John  
; APPLICANT: Parekh, Rajesh Bhikhu  
; APPLICANT: Waterfield, Michael Derek  
; TITLE OF INVENTION: Proteins, Genes, and Their Use for  
; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer  
; FILE REFERENCE: 2543-1-024  
; CURRENT APPLICATION NUMBER: US/09/988,493  
; CURRENT FILING DATE: 2002-05-21  
; PRIOR APPLICATION NUMBER: PCT/GB01/01219  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR FILING DATE: 2000-03-20  
; PRIOR FILING DATE: 2000-03-20  
; PRIOR APPLICATION NUMBER: GB 0006695.1  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 274  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-09-988-493-274

Query Match 49.0%; Score 25; DB 12; Length 14;  
Best Local Similarity 80.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYSN 6  
Db 9 FGYSN 13

## RESULT 15

US-10-014-340-467  
; Sequence 467, Application US/10014340  
; Publication No. US20030064411A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, et al  
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including  
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease  
; FILE REFERENCE: 9195-078  
; CURRENT APPLICATION NUMBER: US/10/014,340  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 823  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 467  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-014-340-467

Query Match 49.0%; Score 25; DB 12; Length 14;  
Best Local Similarity 80.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYSN 6  
Db 9 FGYSN 13

RESULT 16  
US-10-014-340-468  
; Sequence 468, Application US/10014340  
; Publication No. US20030064411A1

; GENERAL INFORMATION:  
; APPLICANT: Herath, et al  
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including  
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease  
; FILE REFERENCE: 9195-078  
; CURRENT APPLICATION NUMBER: US/10/014,340  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 823  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 468  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-014-340-468

Query Match 49.0%; Score 25; DB 12; Length 14;  
Best Local Similarity 80.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYSN 6  
Db 9 FGYSN 13

## RESULT 17

US-09-791-377-526  
; Sequence 526, Application US/09791377  
; Publication No. US20040110938A1  
; GENERAL INFORMATION:  
; APPLICANT: Parekh, Rajesh  
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF  
; TITLE OF INVENTION: SCHIZOPHRENIA  
; FILE REFERENCE: 9195-060-999  
; CURRENT APPLICATION NUMBER: US/09/791,377  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 09/750,395  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 677  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 526  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-377-526

Query Match 49.0%; Score 25; DB 12; Length 14;  
Best Local Similarity 80.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYSN 6  
Db 9 FGYSN 13

## RESULT 18

US-10-255-679-60  
; Sequence 60, Application US/10255679  
; Publication No. US20030069175A1  
; GENERAL INFORMATION:  
; APPLICANT: BAB, ITAI  
; APPLICANT: GAZIT, DAN  
; APPLICANT: YU-CHEN, CHEN  
; APPLICANT: MOHURAD, ANDRAS  
; APPLICANT: SHTEYER, ARIE  
; APPLICANT: CHOREV, MICHAEL  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND PSEUDOPEPTIDES HAVING OSTEOGENIC  
; TITLE OF INVENTION: ACTIVITY AND PHARMACEUTICAL COMPOSITIONS CONTAINING THE  
; FILE REFERENCE: 331949-140798  
; CURRENT APPLICATION NUMBER: US/10/255,679  
; CURRENT FILING DATE: 2002-09-27  
; PRIOR APPLICATION NUMBER: US/09/150,621  
; PRIOR FILING DATE: 1998-09-10

PRIOR APPLICATION NUMBER: PCT/IL97/00087  
PRIOR FILING DATE: 1997-03-10  
PRIOR APPLICATION NUMBER: 117426  
PRIOR FILING DATE: 1996-03-10  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 60  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-255-679-60

Query Match 49.0%; Score 25; DB 14; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGY 4  
|||  
Db 2 GFGY 5

RESULT 19  
US-10-264-309-240  
Sequence 240, Application US/10264309  
Publication No. US20040022794A1  
GENERAL INFORMATION:  
APPLICANT: DURHAM, L. KATHRYN  
APPLICANT: FRIEDMAN, DAVID L.  
APPLICANT: HERATH, HERATH  
APPLICANT: KIMMEL, LIDA H.  
APPLICANT: PAREKH, RAJESH B.  
APPLICANT: POTTER, DAVID M.  
APPLICANT: ROHLF, CHRISTIAN  
APPLICANT: SLIBER, B. MICHAEL  
APPLICANT: SNYDER, PETER J.  
APPLICANT: SOARES, HOLLY D.  
APPLICANT: STIGER, THOMAS R.  
APPLICANT: SUNDERLAND, P. TREY  
APPLICANT: TOWNSEND, ROBERT R.  
APPLICANT: WHITE, W. FROST  
APPLICANT: WILLIAMS, STEPHEN A.  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,  
TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE  
FILE REFERENCE: POA-002.01  
CURRENT APPLICATION NUMBER: US/10/264,309  
CURRENT FILING DATE: 2002-10-03  
PRIOR APPLICATION NUMBER: 60/326,708  
PRIOR FILING DATE: 2001-10-03  
NUMBER OF SEQ ID NOS: 491  
SOFTWARE: PatentIn Version 2.1  
SEQ ID NO 240  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-264-309-240

Query Match 49.0%; Score 25; DB 16; Length 14;  
Best Local Similarity 80.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYKN 6  
|||  
Db 9 FGYSN 13

RESULT 20  
US-09-780-053-158  
Sequence 158, Application US/09780053  
Patent No. US20020102640A1  
GENERAL INFORMATION:

APPLICANT: Rene S. Hubert  
APPLICANT: Daniel E.H. Afar  
APPLICANT: Pia M. Challita-Eid  
APPLICANT: Mary Faris  
APPLICANT: Eliana Levin  
APPLICANT: Steve Chappell Mitchell  
TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
FILE REFERENCE: 129.5USU1  
CURRENT APPLICATION NUMBER: US/09/780,053  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/181,261  
PRIOR FILING DATE: 2000-02-09  
NUMBER OF SEQ ID NOS: 716  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 158  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-09-780-053-158

Query Match 47.1%; Score 24; DB 9; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKNSKF 9  
||:|  
Db 1 GHQNSTF 7

RESULT 21  
US-10-057-475B-10940  
Sequence 10940, Application US/10057475B  
Publication No. US20040002068A1  
GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander  
APPLICANT: Algate, Paul A.  
APPLICANT: Mannion, Jane  
APPLICANT: Clapper, Jonathan David  
APPLICANT: Wang, Aijun  
APPLICANT: Ordonez, Nadia  
APPLICANT: Carter, Lauren  
APPLICANT: McNeill, Patricia Dianne  
APPLICANT: Corixa Corporation  
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
TITLE OF INVENTION: Hematological Malignancies  
FILE REFERENCE: 014058-014402US  
CURRENT APPLICATION NUMBER: US/10/057,475B  
CURRENT FILING DATE: 2002-01-22  
PRIOR APPLICATION NUMBER: US 60/186,126  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US 60/190,479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: US 60/200,545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 60/200,303  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: US 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 60/222,903  
PRIOR FILING DATE: 2000-08-03  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 10979  
SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10940  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Ly1484 short MHC HLA A3 class I binding peptide  
US-10-057-475B-10940

Query Match 47.1%; Score 24; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGK 5  
|||  
Db 6 FGK 9

## RESULT 22

US-10-154-884B-10940  
; Sequence 10940, Application US/10154884B  
; Publication No. US20040005561A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; TITLE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-013521US  
; CURRENT APPLICATION NUMBER: US/10/154, 884B  
; CURRENT FILING DATE: 2002-05-23  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 11290  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10940  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Ly1484 short MHC HLA A3 class I binding peptide  
US-10-154-884B-10940

Query Match 47.1%; Score 24; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGK 5  
|||  
Db 6 FGK 9

## RESULT 23

US-09-780-053-180  
; Sequence 180, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 180  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-180

Query Match 47.1%; Score 24; DB 9; Length 10;  
Best Local Similarity 57.1%; Pred. No. 6.9e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKSKF 9  
|:|:|  
Db 2 GHONSTF 8

## RESULT 24

US-09-780-053-304  
; Sequence 304, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 304  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-304

Query Match 47.1%; Score 24; DB 9; Length 10;  
Best Local Similarity 57.1%; Pred. No. 6.9e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKSKF 9  
|:|:|  
Db 1 GHONSTF 7

## RESULT 25

US-09-780-053-399

```
; Sequence 399, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.SUSU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 399
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-399
```

```
Query Match 47.1%; Score 24; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 GYKNSKF 9
DB 1 GHQNSTF 7
```

```
RESULT 26
US-09-780-053-472
; Sequence 472, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.SUSU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 472
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-472
```

```
Query Match 47.1%; Score 24; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 GYKNSKF 9
DB 4 GHQNSTF 10
```

```
RESULT 27
US-10-319-340-8
; Sequence 8, Application US/10319340
```

```
; Publication No. US20030144211A1
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: McEvey, Rodger P.
; APPLICANT: Geng, Jian-Guo
; TITLE OF INVENTION: Peptide Inhibitors of Inflammation Mediated by Selectins
; FILE REFERENCE: CTC 102 CON DIV
; CURRENT APPLICATION NUMBER: US/10/319,340
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 08/135,319
; PRIOR FILING DATE: 1993-10-12
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic inhibitory peptide
US-10-319-340-8
```

```
Query Match 47.1%; Score 24; DB 14; Length 10;
Best Local Similarity 80.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 YKNSK 8
DB 1 YKNSK 5
```

```
RESULT 28
US-10-013-815-35
; Sequence 35, Application US/10013815
; Publication No. US20030105000A1
; GENERAL INFORMATION:
; APPLICANT: Pero, Stephanie
; APPLICANT: Krag, David
; APPLICANT: Oligino, Lynn
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING GRB7
; FILE REFERENCE: V0139/7048 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/013,815
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/245,755
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of G7BP-4
US-10-013-815-35
```

```
Query Match 47.1%; Score 24; DB 14; Length 11;
Best Local Similarity 80.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 FGYKN 6
DB 3 FGYAN 7
```

```
RESULT 29
US-10-013-815-38
; Sequence 38, Application US/10013815
; Publication No. US20030105000A1
; GENERAL INFORMATION:
; APPLICANT: Pero, Stephanie
; APPLICANT: Krag, David
; APPLICANT: Oligino, Lynn
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING GRB7
; FILE REFERENCE: V0139/7048 (HCL/MAT)
```

/ CURRENT APPLICATION NUMBER: US/10/013,815  
/ CURRENT FILING DATE: 2001-11-05  
/ PRIOR APPLICATION NUMBER: US 60/245,755  
/ PRIOR FILING DATE: 2000-11-03  
/ NUMBER OF SEQ ID NOS: 194  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 38  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Variant of G7BP-4  
US-10-013-815-38

Query Match 47.1%; Score 24; DB 14; Length 11;  
Best Local Similarity 80.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 FGYN 6  
|||  
Db 3 FGYN 7

RESULT 30  
US-10-014-485A-116  
/ Sequence 116, Application US/10014485A  
/ Publication No. US20020168684A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Cell Signaling Technology, Inc.  
/ APPLICANT: COMB, Michael J.  
/ APPLICANT: ZHANG, Hui  
/ APPLICANT: TAN, Yi  
/ TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIES U  
/ FILE REFERENCE: CST-138 CIP2  
/ CURRENT APPLICATION NUMBER: US/10/014,485A  
/ CURRENT FILING DATE: 2002-03-18  
/ PRIOR APPLICATION NUMBER: US 09/148,712  
/ PRIOR FILING DATE: 1998-09-04  
/ PRIOR APPLICATION NUMBER: US 09/535,364  
/ PRIOR FILING DATE: 2000-03-24  
/ NUMBER OF SEQ ID NOS: 145  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 116  
/ LENGTH: 8  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: MOD RES  
/ LOCATION: (5)-(5)  
/ OTHER INFORMATION: PHOSPHORYLATION; serine at position 5 is phosphorylated  
US-10-014-485A-116

Query Match 45.1%; Score 23; DB 13; Length 8;  
Best Local Similarity 80.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 GYKNS 7  
|||  
Db 1 GYKNS 5

RESULT 31  
US-10-387-486-10  
/ Sequence 10, Application US/10387486  
/ Publication No. US20040001867A1  
/ GENERAL INFORMATION:  
/ APPLICANT: INSTITUT PASTEUR  
/ APPLICANT: CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE  
/ TITLE OF INVENTION: VECTORS FOR MOLECULE DELIVERY TO CD11b EXPRESSING CELLS  
/ FILE REFERENCE: B4669A-AD/DBO  
/ CURRENT APPLICATION NUMBER: US/10/387,486  
/ CURRENT FILING DATE: 2003-03-14

/ PRIOR APPLICATION NUMBER: PCT/EP 01/11315  
/ PRIOR FILING DATE: 2001-09-14  
/ PRIOR APPLICATION NUMBER: EP 00402562.3  
/ PRIOR FILING DATE: 2000-09-15  
/ NUMBER OF SEQ ID NOS: 11  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 10  
/ LENGTH: 8  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: intergenic  
/ OTHER INFORMATION: region  
US-10-387-486-10

Query Match 45.1%; Score 23; DB 15; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.2e+06;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GYKNSKF 9  
|||  
Db 2 GYKNSKF 8

RESULT 32  
US-09-879-957-63  
/ Sequence 63, Application US/09879957  
/ Patent No. US20020034755A1  
/ GENERAL INFORMATION:  
/ APPLICANT: SPARKS, Andrew B.  
/ HOFFMAN, No. US20020034755A1h  
/ KAY, Brian K.  
/ FOWLES, Dana M.  
/ MCCONNELL, Stephen J.  
/ TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
/ DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
/ USING SAME  
/ NUMBER OF SEQUENCES: 227  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Pennie & Edmonds LLP  
/ STREET: 1155 Avenue of the Americas  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10036-2711  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/879,957  
/ FILING DATE: 13-Jun-2001  
/ CLASSIFICATION: <Unknown>  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/630,915  
/ FILING DATE: 03-APR-1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Mistock, S. Leslie  
/ REGISTRATION NUMBER: 18,872  
/ REFERENCE/DOCKET NUMBER: 1101-174  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212) 790-9090  
/ TELEFAX: (212) 869-8644/9741  
/ TELEX: 66141 PENNIE  
/ INFORMATION FOR SEQ ID NO: 63:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 9 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: <Unknown>  
/ TOPOLOGY: unknown  
/ MOLECULE TYPE: peptide  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 63:

US-09-879-957-63

Query Match 45.1%; Score 23; DB 9; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKN 6  
| | | | |  
Db 1 GDGYON 6

RESULT 33

US-10-460-512-6  
; Sequence 6, Application US/10460512  
; Publication No. US20040038271A1  
; GENERAL INFORMATION:  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Aya Jakobovits  
; APPLICANT: Arthur B. Raitano  
; TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE  
; TITLE OF INVENTION: ANTIGEN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF  
; FILE REFERENCE: 129.20USU1  
; CURRENT APPLICATION NUMBER: US/10/460,512  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: US/09/638,203  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/148,935  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-460-512-6

Query Match 45.1%; Score 23; DB 12; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKN 7  
| | | | |  
Db 3 GFTYKTA 9

RESULT 34

US-10-460-512-28  
; Sequence 28, Application US/10460512  
; Publication No. US20040038271A1  
; GENERAL INFORMATION:  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Aya Jakobovits  
; APPLICANT: Arthur B. Raitano  
; TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE  
; TITLE OF INVENTION: ANTIGEN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF  
; FILE REFERENCE: 129.20USU1  
; CURRENT APPLICATION NUMBER: US/10/460,512  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: US/09/638,203  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/148,935  
; PRIOR FILING DATE: 1999-08-12  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-460-512-28

Query Match 45.1%; Score 23; DB 12; Length 9;

Best Local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKN 7  
| | | | |  
Db 3 GFTYKTA 9

RESULT 35

US-10-003-983B-11  
; Sequence 11, Application US/10003983B  
; Publication No. US20030103946A1  
; GENERAL INFORMATION:  
; APPLICANT: Imperial College Innovations  
; APPLICANT: Staus, Hans Josef  
; APPLICANT: Amrolia, Persis Jal  
; TITLE OF INVENTION: Immunotherapeutic Methods and Molecules  
; FILE REFERENCE: ICI 103  
; CURRENT APPLICATION NUMBER: US/10/003,983B  
; CURRENT FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-10-003-983B-11

Query Match 45.1%; Score 23; DB 14; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 YKSKRF 9  
| | | | |  
Db 3 YNNHKE 8

RESULT 36

US-10-807-856-63  
; Sequence 63, Application US/10807856  
; Publication No. US20040157216A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: HOFFMAN, Noah  
; APPLICANT: KAY, Brian K.  
; APPLICANT: FOWLKES, Dana M.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; USING SAME  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/807,856  
; FILING DATE: 23-Mar-2004  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,915  
; FILING DATE: 03-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872



REFERENCE/DOCKET NUMBER: 1101-174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 63:  
US-10-807-856-63

Query Match 45.1%; Score 23; DB 16; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKN 6  
| | | | |  
Db 1 GDGYQN 6

## RESULT 37

US-09-572-270A-623  
Sequence 623, Application US/095722270A  
Publication No. US20030148368A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Inter- complementary peptide listing  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/572,270A  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 1144  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 623  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Arabidopsis Thaliana  
OTHER INFORMATION: Sequence located in Unknown at 192-201 and may interact with  
US-09-572-270A-623

Query Match 45.1%; Score 23; DB 10; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKN 6  
| | | | |  
Db 4 GGGFKN 9

## RESULT 38

US-10-317-550-2  
Sequence 2, Application US/10317550  
Publication No. US20030166034A1  
GENERAL INFORMATION:  
APPLICANT: Thomas, George  
TITLE OF INVENTION: P70-S6K or Related Kinase With  
Constitutive Activity  
FILE REFERENCE: 4-20793/A/PCT  
CURRENT APPLICATION NUMBER: US/10/317,550  
CURRENT FILING DATE: 2002-12-12  
PRIOR APPLICATION NUMBER: US/09/297,404B  
PRIOR FILING DATE: 2002-06-04  
NUMBER OF SEQ ID NOS: 24  
SEQ ID NO 2  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Oryctolagus cuniculus  
US-10-317-550-2

Query Match 45.1%; Score 23; DB 14; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYKN 6  
| | | | |  
Db 4 GFSYVN 9

## RESULT 39

US-10-302-100B-28  
Sequence 28, Application US/10302100B  
Publication No. US20040054131A1  
GENERAL INFORMATION:  
APPLICANT: Ballinger, Marcus  
TITLE OF INVENTION: Synthetic Peptides Having FGF Receptor  
TITLE OF INVENTION: Affinity  
FILE REFERENCE: 035784/263218  
CURRENT APPLICATION NUMBER: US/10/302,100B  
CURRENT FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: 09/407,687  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: 60/102,667  
PRIOR FILING DATE: 1998-09-30  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 28  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-10-302-100B-28

Query Match 45.1%; Score 23; DB 12; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1.3e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YKNSKF 9  
| | | | |  
Db 2 YENSPF 7

## RESULT 40

US-10-474-601-12  
Sequence 12, Application US/10474601  
Publication No. US20040158061A1  
GENERAL INFORMATION:  
APPLICANT: Friedrich, Thomas  
APPLICANT: Zimmerman, Norbert  
TITLE OF INVENTION: Reaction of (di)amines in the presence  
of a lysin oxidase and of a reducing agent  
FILE REFERENCE: BGI-156US  
CURRENT APPLICATION NUMBER: US/10/474,601  
CURRENT FILING DATE: 2003-10-09  
PRIOR APPLICATION NUMBER: PCT/EP02/03873  
PRIOR FILING DATE: 2003-10-09  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Pichia pastoris  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: 8  
OTHER INFORMATION: Xaa = Any Amino Acid, probably Ser  
NAME/KEY: VARIANT  
LOCATION: 11  
OTHER INFORMATION: Xaa = Phe or Glu

US-10-474-601-12

Query Match  
Best Local Similarity 45.1%; Score 23; DB 16; Length 12;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKNSKF 9  
Db 1 GYPNAEY 7

RESULT 41

US-10-174-105A-153  
; Sequence 153, Application US/10174105A  
; Publication No. US20030068652A1  
; GENERAL INFORMATION:  
; APPLICANT: Cell Signaling Technology, Inc.  
; APPLICANT: ZHANG, Hui  
; APPLICANT: COMB, Michael J.  
; APPLICANT: TAN, Yi  
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,  
; TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING  
; FILE REFERENCE: CST-138 CIP3  
; CURRENT APPLICATION NUMBER: US/10/174,105A  
; PRIOR FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: US 09/148,712  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: US 09/535,364  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 193  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 153  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: (8)..(8)  
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated  
US-10-174-105A-153

Query Match  
Best Local Similarity 45.1%; Score 23; DB 14; Length 13;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKNS 7  
Db 4 GWKNS 8

RESULT 42

US-10-351-641-919  
; Sequence 919, Application US/10351641  
; Publication No. US20030186874A1  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Arner, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; TITLE OF INVENTION: PROPERTIES  
; FILE REFERENCE: 7872-100  
; CURRENT APPLICATION NUMBER: US/10/351,641  
; PRIOR FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: 09/350,641  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/315,304  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1757  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 919  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-10-351-641-919

Query Match  
Best Local Similarity 43.1%; Score 22; DB 14; Length 8;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGKY 4  
Db 4 GYGY 7

RESULT 43

US-09-799-250-154  
; Sequence 154, Application US/09799250  
; Publication No. US20030032087A1  
; GENERAL INFORMATION:  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Mary Faris  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 121P1F1: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.34US01  
; CURRENT APPLICATION NUMBER: US/09/799,250  
; PRIOR FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 719  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 154  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-799-250-154

Query Match  
Best Local Similarity 43.1%; Score 22; DB 10; Length 9;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGKNSK 8  
Db 2 FGFEENK 8

RESULT 44

US-09-799-250-235  
; Sequence 235, Application US/09799250  
; Publication No. US20030032087A1  
; GENERAL INFORMATION:  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Mary Faris  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 121P1F1: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.34US01  
; CURRENT APPLICATION NUMBER: US/09/799,250  
; PRIOR FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 719  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 235

; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-799-250-235

Query Match 43.1%; Score 22; DB 10; Length 9;  
Best Local Similarity 42.9%; Pred. No. 1.2e+06;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYKNSK 8  
||:::|  
Db 3 FGFEENK 9

RESULT 45  
US-09-799-250-330  
; Sequence 330, Application US/09799250  
; Publication No. US20030032087A1  
; GENERAL INFORMATION:  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Mary Paris  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.34US01  
; CURRENT APPLICATION NUMBER: US/09/799,250  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 719  
; SOFTWARE: FastSeq for windows Version 4.0  
; SEQ ID NO 330  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-799-250-330

Query Match 43.1%; Score 22; DB 10; Length 9;  
Best Local Similarity 42.9%; Pred. No. 1.2e+06;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYKNSK 8  
||:::|  
Db 3 FGFEENK 9

Search completed: August 30, 2004, 11:04:55  
Job time : 13.0068 secs



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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 3.55743 Seconds  
(without alignments)  
130.609 Million cell updates/sec

Title: US-09-720-469A-3  
Perfect score: 51  
Sequence: 1 GFGYKNSKF 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score    | Query Match | Length | DB ID             | Description        |
|------------|----------|-------------|--------|-------------------|--------------------|
| 1          | 30.58.8  | 12          | 4      | US-09-347-926-13  | Sequence 13, Appl  |
| 2          | 27.52.9  | 8           | 1      | US-08-320-373-76  | Sequence 76, Appl  |
| 3          | 27.52.9  | 12          | 2      | US-08-973-563A-28 | Sequence 28, Appl  |
| 4          | 27.52.9  | 12          | 2      | US-08-973-559-28  | Sequence 28, Appl  |
| 5          | 27.52.9  | 12          | 3      | US-08-993-235-8   | Sequence 8, Appl   |
| 6          | 27.52.9  | 12          | 4      | US-09-226-666-4   | Sequence 4, Appl   |
| 7          | 27.52.9  | 12          | 4      | US-08-993-235-8   | Sequence 8, Appl   |
| 8          | 27.52.9  | 12          | 4      | US-09-613-182-2   | Sequence 2, Appl   |
| 9          | 25.49.0  | 10          | 4      | US-09-649-063-15  | Sequence 15, Appl  |
| 10         | 25.49.0  | 14          | 4      | US-09-150-621-60  | Sequence 60, Appl  |
| 11         | 24.548.0 | 12          | 2      | US-08-973-563A-25 | Sequence 25, Appl  |
| 12         | 24.548.0 | 12          | 2      | US-08-973-559-25  | Sequence 25, Appl  |
| 13         | 24.548.0 | 12          | 2      | US-08-973-559-25  | Sequence 25, Appl  |
| 14         | 24.548.0 | 12          | 2      | US-08-973-559-27  | Sequence 27, Appl  |
| 15         | 24.548.0 | 12          | 3      | US-08-993-235-5   | Sequence 5, Appl   |
| 16         | 24.548.0 | 12          | 3      | US-08-993-235-7   | Sequence 5, Appl   |
| 17         | 24.548.0 | 12          | 4      | US-08-993-235-5   | Sequence 5, Appl   |
| 18         | 24.548.0 | 12          | 4      | US-08-993-235-7   | Sequence 7, Appl   |
| 19         | 24.548.0 | 9           | 4      | US-09-417-608A-86 | Sequence 86, Appl  |
| 20         | 24.47.1  | 9           | 6      | 5217869-104       | Patent No. 5217869 |
| 21         | 24.47.1  | 10          | 4      | US-08-135-319A-8  | Sequence 8, Appl   |
| 22         | 24.47.1  | 11          | 4      | US-09-383-667-29  | Sequence 29, Appl  |
| 23         | 24.47.1  | 12          | 4      | US-09-347-926-9   | Sequence 9, Appl   |
| 24         | 23.546.1 | 9           | 6      | 5217869-103       | Patent No. 5217869 |
| 25         | 23.45.1  | 9           | 1      | US-08-215-805A-3  | Sequence 3, Appl   |
| 26         | 23.45.1  | 9           | 1      | US-08-215-805A-41 | Sequence 41, Appl  |
| 27         | 23.45.1  | 9           | 4      | US-08-630-915A-63 | Sequence 63, Appl  |

|    |    |      |    |   |                    |                    |
|----|----|------|----|---|--------------------|--------------------|
| 28 | 23 | 45.1 | 9  | 4 | US-09-638-203-6    | Sequence 6, Appl   |
| 29 | 23 | 45.1 | 9  | 4 | US-09-638-203-28   | Sequence 28, Appl  |
| 30 | 23 | 45.1 | 9  | 6 | 5217869-115        | Patent No. 5217869 |
| 31 | 23 | 45.1 | 11 | 3 | US-08-855-958-4    | Sequence 4, Appl   |
| 32 | 23 | 45.1 | 11 | 3 | US-08-855-958-9    | Sequence 9, Appl   |
| 33 | 23 | 45.1 | 12 | 3 | US-09-407-687-28   | Sequence 28, Appl  |
| 34 | 23 | 45.1 | 14 | 3 | US-09-254-733-50   | Sequence 50, Appl  |
| 35 | 22 | 43.1 | 8  | 1 | US-08-310-429A-14  | Sequence 14, Appl  |
| 36 | 22 | 43.1 | 8  | 2 | US-08-690-734A-13  | Sequence 13, Appl  |
| 37 | 22 | 43.1 | 8  | 2 | US-08-031-538-30   | Sequence 30, Appl  |
| 38 | 22 | 43.1 | 8  | 3 | US-08-742-185-13   | Sequence 13, Appl  |
| 39 | 22 | 43.1 | 8  | 3 | US-09-082-279B-919 | Sequence 919, App  |
| 40 | 22 | 43.1 | 8  | 4 | US-09-315-304B-919 | Sequence 919, App  |
| 41 | 22 | 43.1 | 8  | 4 | US-09-834-784-919  | Sequence 919, App  |
| 42 | 22 | 43.1 | 8  | 4 | US-09-515-965A-919 | Sequence 919, App  |
| 43 | 22 | 43.1 | 8  | 4 | US-09-350-641C-919 | Sequence 919, App  |
| 44 | 22 | 43.1 | 10 | 3 | US-08-467-580-31   | Sequence 31, Appl  |
| 45 | 22 | 43.1 | 10 | 3 | US-08-990-015-7    | Sequence 7, Appl   |

ALIGNMENTS

RESULT 1  
US-09-347-926-13  
Sequence 13, Application US/09347926  
Patent No. 6440386  
GENERAL INFORMATION:  
APPLICANT: LEUNG, SHUI-ON  
TITLE OF INVENTION: STABILIZED RADIOPHOSPHATE-LABELLED PROTEINS  
FILE REFERENCE: 018733/0936  
CURRENT APPLICATION NUMBER: US/09/347, 926  
CURRENT FILING DATE: 1999-07-06  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-347-926-13

Query Match 58.8%; Score 30; DB 4; Length 12;  
Best Local Similarity 55.6%; Pred. No. 22;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 GFGYKNSKF 9  
DB 4 GFSYTNPEF 12

RESULT 2  
US-08-320-373-76  
Sequence 76, Application US/08320373  
Patent No. 5559025  
GENERAL INFORMATION:  
APPLICANT: Ahorn, Horst  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Sommergruber, Wolfgang  
APPLICANT: Zophel, Andreas  
APPLICANT: Blaas, Dieter  
APPLICANT: Kuchler, Ernst  
APPLICANT: Liebig, Hans-Dieter  
APPLICANT: Skern, Timothy  
TITLE OF INVENTION: Expression of Mature Proteinase 2A, the  
TITLE OF INVENTION: Partial Purification Thereof and Preparation of Substrates  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1225 Connecticut Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA

ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/320,373  
FILING DATE: 11-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/971,619  
FILING DATE: 06-NOV-1992  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 466-0800  
TELEFAX: (202) 833-8716  
TELEX: 248636 SSK  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-320-373-76

Query Match 52.9%; Score 27; DB 1; Length 8;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GEGYKN 6  
|||:|  
Db 1 GEGHON 6

RESULT 3  
US-08-973-563A-28  
Sequence 28, Application US/08973563A  
Patent No. 5885965  
GENERAL INFORMATION:  
APPLICANT: Oppenheim, Frank G.  
APPLICANT: Xu, Tao  
APPLICANT: Spacciapoli, Peter  
APPLICANT: Roberts, F. D.  
APPLICANT: Friden, Philip M.  
TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,563A  
FILING DATE: 07-JUN-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,273  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: PER95-02A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..12  
OTHER INFORMATION: /note= "At least one amino acid  
OTHER INFORMATION: must have a D configuration."  
US-08-973-563A-28

Query Match 52.9%; Score 27; DB 2; Length 12;  
Best Local Similarity 62.5%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGYNKSF 9  
|||:|  
Db 5 FGYNKSF 12

RESULT 4  
US-08-973-559-28  
Sequence 28, Application US/08973559  
Patent No. 5912230  
GENERAL INFORMATION:  
APPLICANT: OPPENHEIM, FRANK G.  
APPLICANT: XU, TAO  
APPLICANT: ROBERTS, F. D.  
APPLICANT: SPACCIAPOLI, PETER  
APPLICANT: FRIDEN, PHILIP M.  
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,559  
FILING DATE: 07-JUN-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/481,888  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: PER95-01A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-973-559-28

Query Match 52.9%; Score 27; DB 2; Length 12;  
Best Local Similarity 62.5%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGYNKSKF 9  
|||  
Db 5 FGYNKSKF 12

## RESULT 5

US-08-993-235-8  
; Sequence 8, Application US/08993235  
; Patent No. 6084064  
; GENERAL INFORMATION:  
; APPLICANT: OPPENHEIM, FRANK G.  
; APPLICANT: ROBERTS, F. DONALD  
; APPLICANT: XU, TAO  
; APPLICANT: SPACCIAPOLI, PETER  
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES  
; FILE REFERENCE: 50032/002001  
; CURRENT APPLICATION NUMBER: US/08/993,235  
; CURRENT FILING DATE: 1997-12-18  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-993-235-8

Query Match 52.9%; Score 27; DB 3; Length 12;  
Best Local Similarity 62.5%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGYNKSKF 9  
|||  
Db 5 FGYNKSKF 12

## RESULT 6

US-09-226-666-4  
; Sequence 4, Application US/09226666A  
; Patent No. 6528488  
; GENERAL INFORMATION:  
; APPLICANT: Spacciapoli, Peter  
; APPLICANT: Rothstein, David M.  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS  
; FILE REFERENCE: 50032/007001  
; CURRENT APPLICATION NUMBER: US/09/226,666A  
; CURRENT FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Derived from Homo sapiens  
US-09-226-666-4

Query Match 52.9%; Score 27; DB 4; Length 12;  
Best Local Similarity 62.5%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGYNKSKF 9  
|||  
Db 5 FGYNKSKF 12

RESULT 7  
US-08-993-235-8  
; Sequence 8, Application US/08993235  
; Patent No. 6531573  
; GENERAL INFORMATION:  
; APPLICANT: OPPENHEIM, FRANK G.

; APPLICANT: ROBERTS, F. DONALD  
; APPLICANT: XU, TAO  
; APPLICANT: SPACCIAPOLI, PETER  
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES  
; FILE REFERENCE: 50032/002001  
; CURRENT APPLICATION NUMBER: US/08/993,235  
; CURRENT FILING DATE: 1997-12-18  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-993-235-8

Query Match 52.9%; Score 27; DB 4; Length 12;  
Best Local Similarity 62.5%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGYNKSKF 9  
|||  
Db 5 FGYNKSKF 12

## RESULT 8

US-09-613-182-2  
; Sequence 2, Application US/09613182  
; Patent No. 6294653  
; GENERAL INFORMATION:  
; APPLICANT: Mayfield, Stephen  
; TITLE OF INVENTION: RNA BINDING PROTEIN AND BINDING SITE USEFUL FOR  
; TITLE OF INVENTION: EXPRESSION OF RECOMBINANT MOLECULES  
; FILE REFERENCE: SCR2177S  
; CURRENT APPLICATION NUMBER: US/09/613,182  
; CURRENT FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: 09/341,550  
; PRIOR FILING DATE: 1999-07-13  
; PRIOR APPLICATION NUMBER: PCT/US98/00840  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: 60/035,955  
; PRIOR FILING DATE: 1997-01-17  
; PRIOR APPLICATION NUMBER: 60/069,400  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Chlamydomonas reinhardtii  
US-09-613-182-2

Query Match 52.9%; Score 27; DB 3; Length 14;  
Best Local Similarity 62.5%; Pred. No. 91;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFGYNKSK 8  
|||  
Db 1 GFGYNKSK 8

RESULT 9  
US-09-649-063-15  
; Sequence 15, Application US/09649063  
; Patent No. 6600022  
; GENERAL INFORMATION:  
; APPLICANT: TORIGOE, Kakuji  
; APPLICANT: USHIO, Shunpei  
; APPLICANT: KUNIKATA, Toshio  
; APPLICANT: KURIMOTO, Masashi

; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BROWDY AND NEIMARK



STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/649,063  
FILING DATE: 29-Aug-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/996,140  
FILING DATE: <Unknown>  
APPLICATION NUMBER: JP 52,526/1997  
FILING DATE: 21-FEB-1997  
APPLICATION NUMBER: JP 163,490/1997  
FILING DATE: 6-JUN-1997  
APPLICATION NUMBER: JP 215,490/1997  
FILING DATE: 28-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: TORIGOE-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal fragment  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-649-063-15  
Query Match 49.0%; Score 25; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GFGY 4  
Db 7 GFGY 10  
RESULT 10  
US-09-150-621-60  
Sequence 60, Application US/09150621  
Patent No. 6479460  
GENERAL INFORMATION:  
APPLICANT: BAB, ITAI  
APPLICANT: GAZIT, DAN  
APPLICANT: YU-CHEN, CHEN  
APPLICANT: MUHLRAD, ANDRAS  
APPLICANT: SHTAYER, ARIE  
APPLICANT: CHOREV, MICHAEL  
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND PSEUDOPEPTIDES HAVING OSTEOGENIC  
TITLE OF INVENTION: ACTIVITY AND PHARMACEUTICAL COMPOSITIONS CONTAINING THE  
TITLE OF INVENTION: SAME  
FILE REFERENCE: 331949-140798  
CURRENT APPLICATION NUMBER: US/09/150,621  
PRIOR APPLICATION NUMBER: 1998-09-10  
PRIOR FILING DATE: 1997-03-10  
PRIOR APPLICATION NUMBER: 117426  
PRIOR FILING DATE: 1996-03-10  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 60  
LENGTH: 14

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-150-621-60  
Query Match 49.0%; Score 25; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GFGY 4  
Db 2 GFGY 5  
RESULT 11  
US-08-973-563A-25  
Sequence 25, Application US/08973563A  
Patent No. 5885965  
GENERAL INFORMATION:  
APPLICANT: Openheim, Frank G.  
APPLICANT: Xu, Tao  
APPLICANT: Spacciapoli, Peter  
APPLICANT: Roberts, F. D.  
APPLICANT: Friden, Philip M.  
TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based  
TITLE OF INVENTION: Peptides  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,563A  
FILING DATE: 07-JUN-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,273  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: PER95-02A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..12  
OTHER INFORMATION: /note= "At least one amino acid  
OTHER INFORMATION: must have a D configuration."  
US-08-973-563A-25  
Query Match 48.0%; Score 24.5; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 FGYNKSF 9  
|||  
Db 5 FGYNKSF 11

## RESULT 12

US-08-973-563A-27  
; Sequence 27, Application US/08973563A  
; Patent No. 5885965  
; GENERAL INFORMATION:  
; APPLICANT: Oppenheim, Frank G.  
; APPLICANT: Xu, Tao  
; APPLICANT: Spacciapoli, Peter  
; APPLICANT: Roberts, F. D.  
; APPLICANT: Friden, Philip M.  
; TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based  
; TITLE OF INVENTION: Peptides  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/973,563A  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,273  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: PER95-02A2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 781-861-6240  
; TELEFAX: 781-861-9540  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 1..12  
; OTHER INFORMATION: /note="At least one amino acid  
; OTHER INFORMATION: must have a D configuration."  
US-08-973-563A-27

Query Match 48.0%; Score 24.5; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 FGYNKSF 9  
|||  
Db 5 FGYNKSF 11

RESULT 13  
US-08-973-559-25  
; Sequence 25, Application US/08973559  
; Patent No. 5912230  
; GENERAL INFORMATION:  
; APPLICANT: OPPENHEIM, FRANK G.

APPLICANT: XU, TAO  
APPLICANT: ROBERTS, F. D.  
APPLICANT: SPACCIAPOLI, PETER  
APPLICANT: FRIDEN, PHILIP M.  
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial  
TITLE OF INVENTION: Histatin-Based Peptides  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,559  
FILING DATE: 07-JUN-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/481,888  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: PER95-01A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-973-559-25

Query Match 48.0%; Score 24.5; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 FGYNKSF 9  
|||  
Db 5 FGYNKSF 11

RESULT 14  
US-08-973-559-27  
; Sequence 27, Application US/08973559  
; Patent No. 5912230  
; GENERAL INFORMATION:  
; APPLICANT: OPPENHEIM, FRANK G.  
; APPLICANT: XU, TAO  
; APPLICANT: ROBERTS, F. D.  
; APPLICANT: SPACCIAPOLI, PETER  
; APPLICANT: FRIDEN, PHILIP M.  
; TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial  
; TITLE OF INVENTION: Histatin-Based Peptides  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

```
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,559
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,888
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: PER95-01A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-973-559-27
```

```
Query Match 48.0%; Score 24.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY 2 FGYNKSF 9
   |||||
Db 5 FGYNK-KF 11
```

```
RESULT 15
US-08-993-235-5
; Sequence 5, Application US/08993235
; Patent No. 6084064
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993,235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-5
```

```
Query Match 48.0%; Score 24.5; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY 2 FGYNKSF 9
   |||||
Db 5 FGYNK-KF 11
```

```
RESULT 16
US-08-993-235-7
; Sequence 7, Application US/08993235
; Patent No. 6084064
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
```

```
; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993,235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-7
```

```
Query Match 48.0%; Score 24.5; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY 2 FGYNKSF 9
   |||||
Db 5 FGYNK-KF 11
```

```
RESULT 17
US-08-993-235-5
; Sequence 5, Application US/08993235
; Patent No. 6531573
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993,235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-5
```

```
Query Match 48.0%; Score 24.5; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY 2 FGYNKSF 9
   |||||
Db 5 FGYNK-KF 11
```

```
RESULT 18
US-08-993-235-7
; Sequence 7, Application US/08993235
; Patent No. 6531573
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993,235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-7
```

```
Query Match          48.0%; Score 24.5; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY      2 FGYNKSF 9
      |||||
      5 FGYNK-KF 11

Db

RESULT 19
US-09-417-608A-86
; Sequence 86, Application US/09417608A
; Patent No. 6686164
; GENERAL INFORMATION:
; APPLICANT: Olsen, Arne
; APPLICANT: Røsgen, Erwin
; APPLICANT: Ernst, Steffen
; TITLE OF INVENTION: Low Allergenic Protein Variants
; FILE REFERENCE: 5676.200-US
; CURRENT APPLICATION NUMBER: US/09/417,608A
; CURRENT FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-417-608A-86

Query Match          47.1%; Score 24; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 YKNSKF 9
      :|||
      3 FSNKSF 8

Db

RESULT 20
5217869-104
; Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO:104:
; LENGTH: 9
5217869-104

Query Match          47.1%; Score 24; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GFGYNSK 8
      ||||
      1 GLGAANSK 8

Db

RESULT 21
US-08-135-319A-8
; Sequence 8, Application US/08135319A
; Patent No. 6528487
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; APPLICANT: McEveyer, Rodger P.
; APPLICANT: Geng, Jian-Guo
; TITLE OF INVENTION: Peptide Inhibitors of Inflammation Mediated by Selectins
; FILE REFERENCE: CTC 102 CON
```

```
; CURRENT APPLICATION NUMBER: US/08/135,319A
; CURRENT FILING DATE: 1993-10-12
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic inhibitory peptide
US-08-135-319A-8

Query Match          47.1%; Score 24; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 YKNSK 8
      ||||
      1 YKNSK 5

Db

RESULT 22
US-09-383-667-29
; Sequence 29, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-29

Query Match          47.1%; Score 24; DB 4; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GFGYK 5
      ||||
      2 GIGYK 6

Db

RESULT 23
US-09-347-926-9
; Sequence 9, Application US/09347926
; Patent No. 6440386
; GENERAL INFORMATION:
; APPLICANT: LEUNG, SHUI-ON
; TITLE OF INVENTION: STABILIZED RADIOPHOSPHATE-LABELLED PROTEINS
; FILE REFERENCE: 018733/0936
; CURRENT APPLICATION NUMBER: US/09/347,926
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-09-347-926-9

Query Match 47.1%; Score 24; DB 4; Length 12;  
Best Local Similarity 66.7%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKN 6  
| |||  
Db 4 GSGYEN 9

## RESULT 24

5217869-103  
; Patent No. 5217869  
; APPLICANT: KAUTAR, LAWRENCE M.  
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC  
; REAGENTS  
; NUMBER OF SEQUENCES: 121  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/255,906  
; FILING DATE: 11-OCT-1988  
; SEQ ID NO:103:  
; LENGTH: 9  
5217869-103

Query Match 46.1%; Score 23.5; DB 6; Length 9;  
Best Local Similarity 85.7%; Pred. No. 3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 3 GYKSKF 9  
| ||||  
Db 1 GY-NSKF 6

## RESULT 25

US-08-215-805A-3  
; Sequence 3, Application US/08215805A  
; Patent No. 5559008  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Yung-Fu  
; TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURRELLA  
; TITLE OF INVENTION: SUIS  
; NUMBER OF SEQUENCES: 84  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
; STREET: Clinton Square, P.O. Box 1051  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/215,805A  
; FILING DATE: 22-MAR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Timian, Susan J.  
; REGISTRATION NUMBER: 34,103  
; REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 263-1636  
; TELEFAX: (716) 263-1600  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

ORIGINAL SOURCE:  
; ORGANISM: Pasteurella suis  
; STRAIN: 5943  
; IMMEDIATE SOURCE:  
; LIBRARY: P. suis DNA in Bacteriophage lambda-dash  
; CLONE: (Lambda)yfc33-37  
US-08-215-805A-3

Query Match 45.1%; Score 23; DB 1; Length 9;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YKSKF 9  
: ||||  
Db 1 FKSKF 6

## RESULT 26

US-08-215-805A-41  
; Sequence 41, Application US/08215805A  
; Patent No. 5559008  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Yung-Fu  
; TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURRELLA  
; TITLE OF INVENTION: SUIS  
; NUMBER OF SEQUENCES: 84  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
; STREET: Clinton Square, P.O. Box 1051  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/215,805A  
; FILING DATE: 22-MAR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Timian, Susan J.  
; REGISTRATION NUMBER: 34,103  
; REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 263-1636  
; TELEFAX: (716) 263-1600  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Actinobacillus pleuropneumoniae

US-08-215-805A-41

Query Match 45.1%; Score 23; DB 1; Length 9;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YKSKF 9  
: ||||  
Db 1 FKSKF 6

## RESULT 27

US-08-630-915A-63  
; Sequence 63, Application US/08630915A  
; Patent No. 6309820

```

;
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-630-915A-63

Query Match          45.1%; Score 23; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GFGYKN 6
      |||:|
Db      1 GDGYQN 6

RESULT 28
US-09-638-203-6
; Sequence 6, Application US/09638203
; Patent No. 6602501
; GENERAL INFORMATION:
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Aya Jakobovits
; APPLICANT: Arthur B. Raitano
; TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE
; TITLE OF INVENTION: ANTIGEN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF
; FILE REFERENCE: 129.20USU1
; CURRENT APPLICATION NUMBER: US/09/638,203
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,935
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
```

```

; ORGANISM: Homo Sapiens
; US-09-638-203-6

Query Match          45.1%; Score 23; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GFGYKNS 7
      |||:|
Db      3 GFTYKTA 9

RESULT 29
US-09-638-203-28
; Sequence 28, Application US/09638203
; Patent No. 6602501
; GENERAL INFORMATION:
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Aya Jakobovits
; APPLICANT: Arthur B. Raitano
; TITLE OF INVENTION: NOVEL C-TYPE LECTIN TRANSMEMBRANE
; TITLE OF INVENTION: ANTIGEN EXPRESSED IN HUMAN PROSTATE CANCER AND USES THEREOF
; FILE REFERENCE: 129.20USU1
; CURRENT APPLICATION NUMBER: US/09/638,203
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,935
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-638-203-28

Query Match          45.1%; Score 23; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GFGYKNS 7
      |||:|
Db      3 GFTYKTA 9

RESULT 30
5217869-115
; Patent No. 5217869
; APPLICANT: KAUFAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO:115
; LENGTH: 9
; 5217869-115

Query Match          45.1%; Score 23; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GFGYKNS 7
      |||:|
Db      1 GFGKHT 7

RESULT 31
US-08-855-958-4
; Sequence 4, Application US/08855958B
; Patent No. 6143723
; GENERAL INFORMATION:
```

APPLICANT: Ramalah, Abbur  
TITLE OF INVENTION: PIGMENTARY AGENT  
FILE REFERENCE: 31446-132213  
CURRENT APPLICATION NUMBER: US/08/855,958B  
CURRENT FILING DATE: 1997-05-14  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 4  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: bFGF fragment  
FEATURE:  
OTHER INFORMATION: cyclo peptide  
US-08-855-958-4

Query Match 45.1%; Score 23; DB 3; Length 11;  
Best Local Similarity 42.9%; Pred. No. 3.9e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKSKF 9  
|::|:  
Db 1 GYRSRKY 7

RESULT 32  
US-08-855-958-9  
Sequence 9, Application US/08855958B  
Patent No. 6143723  
GENERAL INFORMATION:  
APPLICANT: Ramalah, Abbur  
TITLE OF INVENTION: PIGMENTARY AGENT  
FILE REFERENCE: 31446-132213  
CURRENT APPLICATION NUMBER: US/08/855,958B  
CURRENT FILING DATE: 1997-05-14  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 9  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: bFGF fragment  
FEATURE:  
OTHER INFORMATION: cyclo peptide  
US-08-855-958-9

Query Match 45.1%; Score 23; DB 3; Length 11;  
Best Local Similarity 42.9%; Pred. No. 3.9e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKSKF 9  
|::|:  
Db 1 GYRSRKY 7

RESULT 33  
US-09-407-687-28  
Sequence 28, Application US/09407687  
Patent No. 6548634  
GENERAL INFORMATION:  
APPLICANT: Ballinger, Marcus  
APPLICANT: Kavanaugh, Michael  
TITLE OF INVENTION: Synthetic Peptides Having FGF Receptor  
FILE REFERENCE: 1517.001  
CURRENT APPLICATION NUMBER: US/09/407,687  
CURRENT FILING DATE: 1999-09-28  
EARLIER APPLICATION NUMBER: 60/102,667  
EARLIER FILING DATE: 1998-09-30  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 28  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-09-407-687-28

Query Match 45.1%; Score 23; DB 4; Length 12;  
Best Local Similarity 66.7%; Pred. No. 4.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YKSKF 9  
|::|:  
Db 2 YENSPF 7

RESULT 34  
US-09-254-733-50  
Sequence 50, Application US/09254733  
Patent No. 6277596  
GENERAL INFORMATION:  
APPLICANT: WATANABE, MANABU  
APPLICANT: MORIYA, TATSUKI  
APPLICANT: AOYAGI, KAORU  
APPLICANT: SUMIDA, NAOMI  
APPLICANT: MURAKAMI, TAKESHI  
TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE cbh1 GENES ORIGINATING  
TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING  
FILE REFERENCE: 99-0266\*/LC(WMC)/00144  
CURRENT APPLICATION NUMBER: US/09/254,733  
CURRENT FILING DATE: 1999-05-07  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 50  
LENGTH: 14  
TYPE: PRT  
ORGANISM: TRICHODERMA VIRIDE MC300-1  
US-09-254-733-50

Query Match 45.1%; Score 23; DB 3; Length 14;  
Best Local Similarity 44.4%; Pred. No. 4.9e+02;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFGYKSKF 9  
|::|:  
Db 6 GTGFNNGYF 14

RESULT 35  
US-08-310-429A-14  
Sequence 14, Application US/08310429A  
Patent No. 5695935  
GENERAL INFORMATION:  
APPLICANT: Page, David C.  
APPLICANT: Reijo, Renee  
TITLE OF INVENTION: DAZ: A GENE ASSOCIATED WITH AZOOSPERMIA  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/310,429A



FILING DATE: 22-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: WH194-07  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-310-429A-14

Query Match 43.1%; Score 22; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKN 6  
|:|:|  
Db 2 GYGFTVN 7

RESULT 36  
US-08-690-734A-13  
Sequence 13, Application US/08690734A  
Patent No. 5871920  
GENERAL INFORMATION:  
APPLICANT: Page, David C.  
TITLE OF INVENTION: DAZ: A GENE ASSOCIATED WITH AZOOSPERMIA  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,734A  
FILING DATE: 31-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/310,429  
FILING DATE: 22-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: WH194-07A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-690-734A-13

Query Match 43.1%; Score 22; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGYKN 6  
|:|:|  
Db 2 GYGFTVN 7

RESULT 37  
US-08-031-538-30  
Sequence 30, Application US/08031538  
Patent No. 5968817  
GENERAL INFORMATION:  
APPLICANT: Sutcliffe, J Gregor  
APPLICANT: Erlander, Mark G  
APPLICANT: Lovenberg, Timothy W  
TITLE OF INVENTION: HUMAN SEROTONIN RECEPTORS, DNA ENCODING  
TITLE OF INVENTION: THE RECEPTORS, AND USES THEREOF  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Scripps Research Institute, Office of  
ADDRESSEE: Patent Counsel  
STREET: 10666 No. 5968817th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/031,538  
FILING DATE: 19930315  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSP5099P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 2  
OTHER INFORMATION: /note= "Xaa is either Leu or Ile"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 5  
OTHER INFORMATION: /note= "Xaa is either Leu or Ser"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 8  
OTHER INFORMATION: /note= "Xaa is either Leu or Phe"  
US-08-031-538-30

Query Match 43.1%; Score 22; DB 2; Length 8;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKNS 7  
|:|:|  
Db 3 GYKNS 7

RESULT 38  
US-08-742-185-13

```
; Sequence 13, Application US/08742185
; Patent No. 6020476
; GENERAL INFORMATION:
; APPLICANT: Page, David C.
; APPLICANT: Reijo, Renee
; APPLICANT: Saxena, Richa
; APPLICANT: Hawkins, Trevor
; APPLICANT: Reeve, Mary Pat
; TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,185
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/690,734
; FILING DATE: 31-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/310,429
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH194-07A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-742-185-13

Query Match      43.1%; Score 22; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 GFGYKN 6  
|:|:|  
Db 2 GYGfVN 7

RESULT 39  
US-09-082-279B-919  
; Sequence 919, Application US/09082279B  
; Patent No. 6258782  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anwer, Mohamed  
; APPLICANT: Lambert, Dennis  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/082,279B  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515

```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 919
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-082-279B-919

Query Match      43.1%; Score 22; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 GFGY 4  
|:|:|  
Db 4 GYGX 7

RESULT 40  
US-09-315-304B-919  
; Sequence 919, Application US/09315304B  
; Patent No. 6348568  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; TITLE OF INVENTION: PROPERTIES  
; FILE REFERENCE: 7872-052  
; CURRENT APPLICATION NUMBER: US/09/315,304B  
; CURRENT FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1667  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 919  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
; US-09-315-304B-919

Query Match 43.1%; Score 22; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGY 4  
|:|:|  
Db 4 GYGX 7

RESULT 41  
US-09-834-784-919  
; Sequence 919, Application US/09834784  
; Patent No. 6562787  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anwer, Mohamed  
; APPLICANT: Lambert, Dennis  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/834,784  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSeq for Windows Version 3.0

```
; SEQ ID NO 919
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-919
```

```
Query Match          43.1%; Score 22; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GFGY 4
         ||||
Db       4 GYGY 7
```

```
RESULT 42
US-09-515-965A-919
; Sequence 919, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sista, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 919
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-919
```

```
Query Match          43.1%; Score 22; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GFGY 4
         ||||
Db       4 GYGY 7
```

```
RESULT 43
US-09-350-641C-919
; Sequence 919, Application US/09350641C
; Patent No. 6656906
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
```

```
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 919
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-641C-919
```

```
Query Match          43.1%; Score 22; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GFGY 4
         ||||
Db       4 GYGY 7
```

```
RESULT 44
US-08-467-580-31
; Sequence 31, Application US/08467580B
; Patent No. 6001809
; GENERAL INFORMATION:
; APPLICANT: Thorsett, Eugene D
; APPLICANT: Yednock, Theodore A
; APPLICANT: Pleiss, Michael A
; TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
; FILE REFERENCE: 123-US-CIP1
; CURRENT APPLICATION NUMBER: US/08/467,580B
; PRIOR FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/273,055
; EARLIER FILING DATE: 1994-07-11
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: derived from first domain of VCAM-1
US-08-467-580-31
```

```
Query Match          43.1%; Score 22; DB 3; Length 10;
Best Local Similarity 57.1%; Pred. No. 5.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 GFGYKNS 7
         |||::||
Db       2 GFGNEHS 8
```

```
RESULT 45
US-08-990-015-7
; Sequence 7, Application US/08990015A
; Patent No. 6093701
; GENERAL INFORMATION:
; APPLICANT: Budker, Vladimir
; APPLICANT: Hagstrom, James E.
; APPLICANT: Sebestyen, Magdolna G.
; APPLICANT: Wolff, Jon A.
; TITLE OF INVENTION: A METHOD FOR COVALENT ATTACHMENT OF COMPOUNDS TO GENES
; FILE REFERENCE: Covalent Attachment to Genes
; CURRENT APPLICATION NUMBER: US/08/990,015A
; EARLIER FILING DATE: 1997-12-12
; EARLIER APPLICATION NUMBER: 60/050842
; EARLIER FILING DATE: 1997-05-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7
; LENGTH: 10
```

TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CONTAINS  
; OTHER INFORMATION: SEQUENCES FROM THE SV40 GENOME  
US-08-990-015-7

Query Match 43.1%; Score 22; DB 3; Length 10;  
Best Local Similarity 66.7%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GYKNSK 8  
|||  
Db 2 GYKKRK 7

Search completed: August 30, 2004, 10:57:12  
Job time : 4.55743 secs



Db 1 GFGYKNSKF 9

RESULT 2

AAV69924  
ID AAV69924 standard; peptide; 11 AA.  
XX  
AC AAV69924;  
XX

DT 11-APR-2000 (first entry)

DE Human cyclophilin B peptide fragment #4.

KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;  
KW HLA antigen; diagnosis; tumour; therapy.

OS Homo sapiens.

PN WO9967288-A1.

PD 29-DEC-1999.

PF 24-JUN-1999; 99WO-JP003360.

PR 25-JUN-1998; 98JP-00178449.

PA (SUMU) SUMITOMO PHARM CO LTD.  
(ITOH/) ITOH K.

PI Itoh K, Gomi S;

DR WPI; 2000-116932/10.

PT Tumour antigen peptides derived from cyclophilin B for treatment and  
PT diagnosis of tumors.

PS Claim 4; Page 50; 64pp; Japanese.

CC This sequence represents a cyclophilin B peptide of the invention. The  
CC peptides are tumour antigen peptides derived from cyclophilin B, that  
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The  
CC peptides are used for the treatment and diagnosis of tumours

SO Sequence 11 AA;

Query Match 76.5%; Score 39; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GYKNSKF 9  
Db 1 GYKNSKF 7

RESULT 3

ABG70966  
ID ABG70966 standard; peptide; 12 AA.

AC ABG70966;

DT 04-DEC-2002 (first entry)

DE Human protein kinase Cbeta1 peptide.

KW Human; radiotherapeutic agent precursor; targeting peptide; tumour;  
KW phosphorylation peptide; linker; Src homology region 2 domain; SH\_2;  
KW infectious lesion; breast; colon; rectum; prostate; ovary; testes;  
KW pathological lesion; chest; abdomen; pelvis; skin; cardiovascular lesion;  
KW myocardial infarct; atherosclerotic plaque; clot; thrombosis;  
KW pulmonary embolism; inflammatory lesion; hyperplasia;  
KW protein kinase Cbeta1.  
OS Homo sapiens.

PN US6440386-B1.

PD 27-AUG-2002.

PF 06-JUL-1999; 99US-00347926.

PR 06-JUL-1998; 98US-0091736P.

PA (IMMU-) IMMUNOMEDICS INC.

PI Leung S;

DR WPI; 2002-722167/78.

PT Radioactive agent precursor, useful in manufacture of in vivo  
PT radiotherapeutic agents, comprises protein containing targeting peptide,  
PT phosphorylation peptide, linker and Src homology region 2 domain.

PS Disclosure; Col 7; 13pp; English.

CC The present invention relates to a new radiotherapeutic agent precursor  
CC comprising a protein containing a targeting peptide, a phosphorylation  
CC peptide, a linker and Src homology region 2 domain (SH\_2). The invention  
CC is useful for preparing radiotherapeutic agents, useful for the treatment  
CC of tumour and an infectious lesion. The lesions include infectious  
CC lesions of breast, colon, rectum, prostate, ovary and testes;  
CC pathological lesions affecting chest, abdomen and pelvis and skin; and  
CC cardiovascular lesions such as myocardial infarct, atherosclerotic  
CC plaque, clot, thrombosis, pulmonary embolism, inflammatory lesions and  
CC hyperplasia. The linker in the radiotherapeutic agent is long and  
CC sufficiently flexible to allow the SH\_2 domain to make a turn and fold  
CC back on the phosphorylated substrate. Thus, the radiotherapeutic agent  
CC exhibits improved stability in vivo, by avoiding the ready  
CC phosphorylation, while maintaining the binding ability of the agent. The  
CC present amino acid sequence represents a human peptide that contains an  
CC SH\_2 domain as described in the invention

SO Sequence 12 AA;

Query Match 58.8%; Score 30; DB 5; Length 12;  
Best Local Similarity 55.6%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 GFGYKNSKF 9  
Db 4 GFGYKNSKF 12

RESULT 4

ADD44040  
ID ADD44040 standard; peptide; 13 AA.

AC ADD44040;

DT 15-JAN-2004 (first entry)

DE CPG2 peptide #60 with potential human MHC class II binding activity.

KW bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;  
KW immunogenic; T-cell epitope; MHC class II binding ligand;  
KW immunostimulant; enzyme therapy; immune response;  
KW gene directed enzyme prodn strategy; vaccine; enzyme; EC 3.4.17.11.  
OS Pseudomonas sp. RS-16.  
XX WO2003045426-A1.  
XX 05-JUN-2003.  
XX 27-NOV-2002; 2002WO-EP013351.  
XX 29-NOV-2001; 2001EP-00128519.

PR 25-JAN-2002; 2002EP-00001778.  
PR 13-SEP-2002; 2002EP-00020634.  
XX  
XX (MERE ) MERCK PATENT GMBH.  
XX  
PI Hellendoorn K, Baker M, Williams S, Carr FU;  
XX  
XX WPI; 2003-513617/48.  
DR  
XX  
PT New modified bacterial enzyme carboxypeptidase G2 (CPG2) having  
PT substantially non-immunogenic or less immunogenic than any non-modified  
PT CPG2, useful for inducing an immune response in a human host.  
XX  
XX  
PS Claim 3; Page 13; 52pp; English.  
XX  
XX The invention relates to a novel modified bacterial enzyme  
CC carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2  
CC proteins that are substantially non-immunogenic or less immunogenic than  
CC any non-modified CPG2 having essentially the same biological specificity  
CC when used in vivo, and comprising specifically amino acid residues having  
CC alterations compared with the non-modified parochial enzyme. The  
CC alterations cause a reduction or an elimination of one or more of T-cell  
CC epitope sequences, which act in the parental enzyme as MHC class II  
CC binding ligands and stimulate T-cells. The modified CPG2 enzyme and the  
CC CPG2 proteins have immunostimulant activity and may be used in enzyme  
CC therapy. The modified CPG2 enzyme may be used to induce an immune  
CC response in a human host, or as a therapeutic entity such as the gene  
CC directed enzyme prodrg strategy. The peptide is useful for the  
CC manufacture of a modified CPG2 enzyme having substantially no or less  
CC immunogenicity than any non-modified parental enzyme when used in vivo,  
CC and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.  
CC This sequence represents a CPG2 enzyme peptide with potential human MHC  
CC class II binding activity of the invention.  
XX  
SQ Sequence 13 AA;

QY 1 GFGYKNSK 8  
| | | | : |  
Db 2 GFGYHSDK 9

Query Match 58.8%; Score 30; DB 7; Length 13;  
Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 5  
ADD44091  
ID ADD44091 standard; peptide; 13 AA.  
XX  
AC ADD44091;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE CPG2 peptide #111 with potential human MHC class II binding activity.  
XX  
XX bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;  
KW immunogenic; T-cell epitope; MHC class II binding ligand;  
KW immunostimulant; enzyme therapy; immune response;  
KW Gene directed enzyme prodrg strategy; vaccine; enzyme; EC 3.4.17.11.  
XX  
OS Pseudomonas sp. RS-16.  
XX  
XX WO2003045426-A1.  
XX  
XX PD 05-JUN-2003.  
XX  
XX 27-NOV-2002; 2002WO-EP013351.  
XX  
XX 29-NOV-2001; 2001EP-00128519.  
PR 25-JAN-2002; 2002EP-00001778.  
PR 13-SEP-2002; 2002EP-00020634.  
XX  
XX (MERE ) MERCK PATENT GMBH.  
PA

XX  
PI Hellendoorn K, Baker M, Williams S, Carr FU;  
XX  
XX WPI; 2003-513617/48.  
DR  
XX  
PT New modified bacterial enzyme carboxypeptidase G2 (CPG2) having  
PT substantially non-immunogenic or less immunogenic than any non-modified  
PT CPG2, useful for inducing an immune response in a human host.  
XX  
XX  
PS Claim 3; Page 13; 52pp; English.  
XX  
XX The invention relates to a novel modified bacterial enzyme  
CC carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2  
CC proteins that are substantially non-immunogenic or less immunogenic than  
CC any non-modified CPG2 having essentially the same biological specificity  
CC when used in vivo, and comprising specifically amino acid residues having  
CC alterations compared with the non-modified parochial enzyme. The  
CC alterations cause a reduction or an elimination of one or more of T-cell  
CC epitope sequences, which act in the parental enzyme as MHC class II  
CC binding ligands and stimulate T-cells. The modified CPG2 enzyme and the  
CC CPG2 proteins have immunostimulant activity and may be used in enzyme  
CC therapy. The modified CPG2 enzyme may be used to induce an immune  
CC response in a human host, or as a therapeutic entity such as the gene  
CC directed enzyme prodrg strategy. The peptide is useful for the  
CC manufacture of a modified CPG2 enzyme having substantially no or less  
CC immunogenicity than any non-modified parental enzyme when used in vivo,  
CC and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.  
CC This sequence represents a CPG2 enzyme peptide with potential human MHC  
CC class II binding activity of the invention.  
XX  
SQ Sequence 13 AA;

QY 1 GFGYKNSK 8  
| | | | : |  
Db 5 GFGYHSDK 12

Query Match 58.8%; Score 30; DB 7; Length 13;  
Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 6  
AAR72924  
ID AAR72924 standard; peptide; 8 AA.  
XX  
AC AAR72924;  
XX  
DT 16-OCT-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 29-NOV-1995 (first entry)  
XX  
DE Yeast PPIase tryptic fragment 4.  
XX  
XX Escherichia coli; protein conformation; folding; acceleration;  
KW PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;  
KW isomerisation; prolyl peptide bond.  
XX  
OS Saccharomyces cerevisiae; strain AH22.  
XX  
XX EP647714-A1.  
XX  
XX 12-APR-1995.  
XX  
XX 19-JUL-1990; 94EP-00203612.  
XX  
XX 19-JUL-1989; 89JP-00184738.  
PR 06-OCT-1989; 89JP-00260244.  
PR 29-DEC-1989; 89JP-00344705.  
PR 19-JUL-1990; 90EP-00307914.  
XX  
XX (TOFU ) TONEN CORP.  
PA  
XX Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;  
PI



XX WPI; 1995-140756/19.  
XX  
XX New E.coli peptidyl prolyl cis trans isomerase beta - used to accelerate  
PT the folding of proteins, partic. for activation of inactive recombinant  
PT proteins.  
XX  
XX Example 2; Page 22; 85pp; English.  
XX  
XX AAR72921-29 are tryptic fragments of a yeast PPIase (peptidyl prolyl cis  
CC trans isomerase). The yeast PPIase has a single mol. wt. of about 17 kDa  
CC and a single isoelectric point of about 6.2. The enzyme catalyses the  
CC isomerisation of prolyl peptide bonds in proteins and accelerates the  
CC folding of the protein. The inventors are claiming a PPIase-beta.  
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to  
CC correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated  
CC on 16-OCT-2003 to standardise OS field)  
XX  
XX Sequence 8 AA;  
SQ  
Query Match 54.9%; Score 28; DB 2; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 GFGYKNS 7  
|||  
1 GFGYAGS 7  
Db  
RESULT 7  
AAR72880  
ID AAR72880 standard; peptide; 8 AA.  
XX  
XX AAR72880;  
AC  
XX  
XX 16-OCT-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 29-NOV-1995 (first entry)  
XX  
XX Yeast PPIase tryptic fragment 4.  
DE  
XX  
XX Escherichia coli; protein conformation; folding; acceleration;  
KM PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;  
KM isomerisation; prolyl peptide bond.  
XX  
XX Saccharomyces cerevisiae; strain AH22.  
OS  
XX  
XX BP647713-A1.  
PN  
XX  
XX 12-APR-1995.  
PD  
XX  
XX 19-JUL-1990; 94EP-00203610.  
PF  
XX  
XX 19-JUL-1989; 89JP-00184738.  
PR 06-OCT-1989; 89JP-00260244.  
PR 29-DEC-1989; 89JP-00344705.  
PR 19-JUL-1990; 90EP-00307914.  
PR  
XX  
XX (TOFU) TONEN CORP.  
PA  
XX  
XX Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;  
PI  
XX  
XX WPI; 1995-140755/19.  
DR  
XX  
XX New E.coli peptidyl prolyl cis trans isomerase alpha - used to accelerate  
PT the folding of proteins, partic. for activation of inactive recombinant  
PT proteins.  
PT  
XX  
XX Example 2; Page 22; 85pp; English.  
XX  
XX AAR72877-85 are tryptic fragments of a yeast PPIase (peptidyl prolyl cis  
CC trans isomerase). The yeast PPIase has a single mol. wt. of about 17 kDa  
CC and a single isoelectric point of about 6.2. The enzyme catalyses the

CC isomerisation of prolyl peptide bonds in proteins and accelerates the  
CC folding of the protein. The inventors are claiming the PPIase-alpha.  
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to  
CC correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated  
CC on 16-OCT-2003 to standardise OS field)  
XX  
XX Sequence 8 AA;  
SQ  
Query Match 54.9%; Score 28; DB 2; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 GFGYKNS 7  
|||  
1 GFGYAGS 7  
Db  
RESULT 8  
AAW33943  
ID AAW33943 standard; peptide; 9 AA.  
XX  
XX AAW33943;  
AC  
XX  
XX 28-MAY-1998 (first entry)  
DT  
XX  
XX Beta1-adrenergic receptor antagonist.  
DE  
XX  
XX Antagonist; integral membrane protein; inhibitor; transmembrane domain;  
KM therapy; psychotic disorder; Huntington's disease; Parkinson's disease;  
KM post-myocardial infarction; HIV infection; cell proliferation disorder;  
KM peptic ulcer; glaucoma; asthma; renal disease; autoimmune disease;  
KM antibacterial; beta1-adrenergic receptor.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9735881-A2.  
PN  
XX  
XX 02-OCT-1997.  
PD  
XX  
XX 26-MAR-1997; 97WO-CA000203.  
PF  
XX  
XX 27-MAR-1996; 96US-0014306P.  
PR 25-JUN-1996; 96US-00670119.  
PR 20-AUG-1996; 96US-0024240P.  
PR  
XX  
XX (NGY/) NG G Y K.  
PA (SEEM/) SEEMAN P.  
PA (GEOR/) GEORGE S R.  
PA (ODOW/) O'DOWD B F.  
PA  
XX  
XX Ng GYK, Seeman P, George SR, Odowd BF;  
PI  
XX  
XX WPI; 1997-489566/45.  
DR  
XX  
XX Inhibitor of integral membrane protein - used to treat e.g.  
PT schizophrenia, hypertension, viral infection, cancer etc.  
PT  
XX  
XX Claim 17; Page 94; 127pp; English.  
PS  
XX  
XX This sequence is a beta1-adrenergic receptor antagonist, and is an  
CC antagonist of the invention. The antagonists (A) are for inhibiting the  
CC function of a prokaryotic or eukaryotic integral membrane protein (IMP)  
CC having at least one transmembrane domain (TMD), comprises a peptide  
CC including at least 4 consecutive amino acids (aa) from the sequence of  
CC the TMD. (A) are used to treat or prevent disorders in mammals that  
CC involve disturbances of IMP, and the same effect is achieved by inserting  
CC a nucleic acid encoding (A) into the cells of the mammal. Specified  
CC conditions that can be treated are schizophrenia, psychotic disorders,  
CC Huntington's disease, Tourette's syndrome, hypertension, post-myocardial  
CC infarction, tachyarrhythmia, human immunodeficiency virus infection, and  
CC AIDS, cell proliferation (cancer, psoriasis or hyperkeratosis), and drug  
CC abuse. (A) can also be used to treat peptic ulcer, glaucoma, asthma,  
CC renal disease, Parkinson's disease, congestive heart failure, migraine,

depression, obesity, diabetic neuropathy/retinopathy, autoimmune diseases, graft rejection etc. (A) can be used as diuretics and antibacterials. (A) may also be used to determine function of orphan receptors and, when attached to a marker, for tissue imaging to localise/quantify specific receptors. The transgenic animals are used to test efficacy/toxicity of (A) and as models of diseases. (A) are very specific and selective, against the IMP from which they are derived, so should have few side effects

Sequence 9 AA;

Query Match 52.9%; Score 27; DB 2; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GYKNSKF 9  
DB 1 GYANSAF 7

RESULT 9  
ABB82364  
ID ABB82364 standard; peptide; 10 AA.

AC ABB82364;

DT 08-JAN-2003 (first entry)

DE BAK protein fragment.

KW BAK; MLL; cytostatic; neuroprotective; nootropic; cerebroprotective; apoptosis; human.

OS Homo sapiens.

PN WO200274908-A2.

PD 26-SEP-2002.

PF 04-MAR-2002; 2002WO-US006757.

PR 02-MAR-2001; 2001US-0273091P.

PA (MDSP-) MDS PROTEOMICS INC.

PI Mcfadden G, Moran MF;

DR WPI; 2002-740855/80.

Identifying agents which may be potentially pro-apoptotic or anti-apoptotic for treating acute and chronic neurodegenerative diseases, comprises determining the effect of the test agent on complexes of BAK and/or MLL proteins.

Disclosure; Page 14; 83pp; English.

The invention relates to identifying agents which may be potentially pro-apoptotic or anti-apoptotic which involves determining the effect of a test agent on the complexes of BAK and/or MLL proteins. The methods are useful for identifying agents which may be potentially pro-apoptotic or anti-apoptotic and for identifying MLL-interacting polypeptides, and in conducting a target or drug discovery system. The methods are useful for identifying agents capable of inhibiting MLL activity or which can mimic the activity of MLL by inhibiting the activity of BAK and which are therefore anti-apoptotic agents. Agents identified by the method as involved in regulation of apoptosis may be used in the development of therapeutic agents and methods, and drug screening assays, and in increasing the sensitivity of cancer cells to chemotherapeutic treatment. Therapeutic applications of apoptosis manipulation include treatment of acute and chronic neurodegenerative diseases, e.g. stroke, Alzheimer's or Huntington's disease by drugs, and sensitization of cancer cells for drug /radiation-induced apoptosis by modulation of survival signals and viral transfer of apoptosis promoting genes. The present sequence represents a

BAK protein fragment  
Sequence 10 AA;

Query Match 52.9%; Score 27; DB 5; Length 10;  
Best Local Similarity 80.0%; Pred. No. 3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFGYK 5  
DB 6 GFGYR 10

RESULT 10  
AAW19418  
ID AAW19418 standard; peptide; 12 AA.

AC AAW19418;

DT 05-SEP-1997 (first entry)

DE Anti-fungal and anti-bacterial histatin-based peptide 113-F4.5.12.

KW Candida albicans; periodontitis; caries; tooth decay; oral infection; vaginal infection; urethral infection; mucosal infection; ear infection; respiratory infection; skin infection; ophthalmic infection; bacterial disease; Streptococcus mutans; Porphyromonas gingivalis; Clostridium histolyticum.

OS Synthetic.

FH Key Location/Qualifiers

FT Region 1..12  
FT /note= "At least one amino acid must have a D-configuration"

PN WO9640768-A2.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009374.

PR 07-JUN-1995; 95US-00481888.

PA (PERI-) PERIODONTIX INC.

PI (UYBO-) UNIV BOSTON.

PI Oppenheim FG, Xu T, Roberts FD, Spacciapoli P, Friden PM;

DR WPI; 1997-052232/05.

Anti-fungal and anti-bacterial histatin-based peptide(s) - useful esp for treating Candidal infections, periodontitis and caries.

Claim 2; Fig 1; 72pp; English.

The present sequence represents a specifically claimed peptide sequence, peptide 113-F4.5.12, where at least one amino acid is in the D-configuration. The peptide preferably is modified by an acetyl or carbamyl addition at the N-terminus and/or amidation at the C-terminus. The peptide, based on the naturally occurring histidine-rich human histatins, have anti-fungal and anti-bacterial activity and are useful in compositions for the treatment of oral, vaginal, urethral, mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial infections. It is particularly effective against local and systemic Candida albicans infection, against oral bacterial diseases such as caries and periodontitis (by inhibiting e.g. Streptococcus mutans and Porphyromonas gingivalis) and against Clostridium histolyticum. The peptide has superior anti-fungal (especially anti-Candidal) and anti-bacterial activity, particularly on a weight basis, compared to the longer, naturally occurring histatins. Peptides containing D-residues are also more resistant to degradation than L-amino acid versions

SQ Sequence 12 AA;

Query Match  
Best Local Similarity 52.9%; Score 27; DB 2; Length 12;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 FGYNKSKF 9  
5 FGYNKSKF 12

Db 5 FGYNKSKF 12

RESULT 11  
AAW19464  
ID AAW19464 standard; peptide; 12 AA.

AC AAW19464;  
DT 05-SEP-1997 (first entry)

DE Anti-fungal and anti-bacterial D-amino acid peptide 113-F4.5.12.

XX Candida albicans; periodontitis; caries; tooth decay; oral infection;  
KW vaginal infection; urethral infection; mucosal infection; ear infection;  
KW respiratory infection; skin infection; ophthalmic infection;  
KW bacterial disease; Streptococcus mutans; Porphyromonas gingivalis;  
KW Clostridium histolyticum.

XX Synthetic.

XX OS  
XX FH Key Location/Qualifiers  
XX FT Region 1..12  
XX FT /note= "At least one amino acid must have D-configuration"

XX WO9640770-A2.  
XX PD 19-DEC-1996.  
XX PF 07-JUN-1996; 96WO-US009962.  
XX PR 07-JUN-1995; 95US-00485273.  
XX PA (PERI-) PERIODONTIX INC.  
XX PA (UYBO-) UNIV BOSTON.  
XX PI Oppenheim FG, Xu T, Spacciapoli P, Roberts FD, Friden PM;  
XX WPI; 1997-052234/05.  
XX DR  
XX PT Anti-fungal and anti-bacterial D-amino acid histatins and histatin-based  
XX PT peptide(s) - useful esp for treating Candidal infections, periodontitis  
XX PT and caries.  
XX PS Claim 2; Fig 1; 63pp; English.

CC The present sequence represents a specifically claimed example of an anti-fungal and anti-bacterial D-amino acid histatin-based peptide 113-F4.5.12, where at least one amino acid in the peptide is in the D-configuration. The peptide is preferably modified by an acetyl or carbamyl addition at the N-terminus and/or amidation at the C-terminus. The novel D-amino acid-containing peptide, based on the naturally occurring histidine-rich human histatins, have anti-fungal and anti-bacterial activity and are useful in compositions for the treatment of oral, vaginal, urethral, mucosal, respiratory, skin, ear and ophthalmic fungal or bacterial infections. It is particularly effective against local and systemic Candida albicans infection, against oral bacterial diseases such as caries and periodontitis (by inhibiting e.g. Streptococcus mutans and Porphyromonas gingivalis) and against Clostridium histolyticum. The D-amino acid-containing peptide has superior anti-fungal (especially anti-candidal) and anti-bacterial activity, particularly on a weight basis, compared to the natural L-amino acid forms of histatins and histatin-based peptides. The presence of D-residues also makes the peptides more resistant to degradation than

CC corresponding L-amino acid versions  
XX SQ Sequence 12 AA;

Query Match  
Best Local Similarity 52.9%; Score 27; DB 2; Length 12;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 FGYNKSKF 9  
5 FGYNKSKF 12

Db 5 FGYNKSKF 12

RESULT 12  
AAV25144  
ID AAV25144 standard; peptide; 12 AA.

AC AAV25144;  
DT 27-AUG-1999 (first entry)

DE Antibacterial and antifungal peptide 5.

XX Antifungal; antibacterial; treatment; infection; candidal; ophthalmic;  
KW viral vaginal; urethral; mucosal; respiratory; skin; ear; oral.

XX Unidentified.

XX OS  
XX PN WO9931123-A1.  
XX PD 24-JUN-1999.  
XX PF 14-DEC-1998; 98WO-US026513.  
XX PR 18-DEC-1997; 97US-00993235.  
XX PA (PERI-) PERIODONTIX INC.  
XX PA (UYBO-) UNIV BOSTON.  
XX PI Roberts FD, Spacciapoli P, Friden PM, Oppenheim FG, Xu T;  
XX WPI; 1999-395161/33.  
XX DR  
XX PT Antibacterial and antifungal peptides.  
XX PS Disclosure; Page 8; 31pp; English.

CC This invention describes novel substantially pure antibacterial and antifungal peptides (A) containing between 13 and 20 amino acids, where the peptide has the amino acid sequence: R1-R2-R3-R4-R5-R6-R7-R8-R9-R10-R11-R12-R13-R14-R15-R16-R17-R18-R19-R20-R21-R22-R23; where: R1 is Asp or absent; R2 and R20 are Ser or absent; R3, R18, R19 and R21 are His or absent; R4 is Ala, R5, R6, R9, R12, R13, are Lys, Gln, Arg or another basic amino acid; R7, R8 and R15 are His, Phe, Tyr, Leu, another hydrophobic amino acid, or is absent; R10 is Tyr; R16 is Glu or absent; R17 is Lys or absent; R22 is Arg or absent; R23 is Gly or absent; where Gln cannot simultaneously occupy positions R5, R6, R12, and R13 of the amino acid sequence. (A) can be used to treat fungal or bacterial infection in a mammal. The peptides are particularly used to treat candidal infection, as well as bacterial and viral infections, especially vaginal, urethral, mucosal, respiratory, skin, ear, oral, or ophthalmic infections. The infections that can be treated include those caused by Candida albicans, Actinomyces actinomycetemcomitans, Actinomyces viscosus, Bacterioides forsythus, Bacterioides gracilis, Bacterioides ureolyticus, Campylobacter concisus, Campylobacter rectus, Campylobacter showae, Campylobacter sputorum, Capnocytophaga gingivalis, Capnocytophaga ochracea, Capnocytophaga sputigena, Clostridium histolyticum, Bikenella corrodens, Eubacterium nodatum, Fusobacterium nucleatum, Fusobacterium periodonticum, Peptostreptococcus nigros, Porphyromonas endodontalis, Porphyromonas gingivalis, Prevotella intermedia, Prevotella nigrescens, Propionibacterium acnes, Pseudomonas aeruginosa, and those caused by various staphylococcal and streptococcal species. AAV25140-Y25149 are peptides used in the description of the invention

XX SQ Sequence 12 AA;  
Query Match 52.9%; Score 27; DB 2; Length 12;  
Best Local Similarity 62.5%; Pred. No. 3.6e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 2 FGYNKSKF 9  
| | | | |  
5 FGYNKSKF 12  
DB  
RESULT 13  
AAB11978  
ID AAB11978 standard; peptide; 12 AA.  
XX AC AAB11978;  
XX DT 24-NOV-2000 (first entry)  
XX DE Histatin-related peptide, P-113-F4.5.12.  
XX KW Histatin-related peptide; cystic fibrosis; Pseudomonas aeruginosa;  
XX KM antibiotic resistance; pulmonary infection; antibacterial; antibiotic.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WO200040204-A2.  
XX PD 13-JUL-2000.  
XX PF 07-JAN-2000; 2000WO-US0000480.  
XX PR 08-JAN-1999; 99US-00226666.  
XX PA (PERI-) PERIODONTIX INC.  
XX PI Spacciapoli P, Rothstein DM, Friden PM;  
XX DR WPI; 2000-465852/40.  
XX PT Treating cystic fibrosis and combating Pseudomonas and other pulmonary  
XX PT infections in a mammal comprises administering histatin or a fragment of  
XX PT it.  
XX PS Claim 32; Page 19; 27pp; English.  
XX  
CC The invention relates to treating cystic fibrosis via the administration  
CC of a histatin, a fragment of histatin, or a histatin-related peptide. The  
CC peptide that is administered contains between 8 and 20 amino acids and  
CC has the sequence: X1-X2-X3-X4-X5-X6-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16-  
CC X17-X18-X19-X20-X21-X22-X23 where X1 is Asp or absent; X2 is Ser or  
CC absent; X3 is His or absent; X4 is Ala, His, Leu or absent; X5 is Lys,  
CC Gln, Arg, Orn, or another basic amino acid; X6 is Arg, Gln, Lys, or  
CC another basic amino acid; X7 is His, Phe, Tyr, Leu, or another hydrophobic  
CC amino acid; X8 is His, Phe, Tyr, Leu, or another hydrophobic amino acid;  
CC X9 is Gly, Lys, Arg, Ser, or a basic amino acid; X10 is Tyr; X11 is Lys,  
CC His, Phe, Leu, or another hydrophobic amino acid; X12 is Lys, Gln, Arg,  
CC Orn, or another basic amino acid; X13 is Lys, Gln, Arg, Orn, another  
CC basic amino acid, or absent; X14 is Phe or absent; X15 is His, Phe, Tyr,  
CC Leu, another hydrophobic amino acid, or absent; X16 is Glu or absent; X17  
CC is Lys or absent; X18 is His or absent; X19 is His or absent; X20 is Ser  
CC or absent; X21 is His or absent; X22 is Arg or absent; and X23 is Gly or  
CC absent. Optionally, the peptide may contain at least one modification  
CC selected from an N-terminal acyl addition, an N-terminal carbamyl  
CC addition and a C-terminal amide addition. Histatin, histatin fragments  
CC and histatin-related peptides have activity against Pseudomonas  
CC aeruginosa. They may therefore be used to combat Pseudomonas infections  
CC and other pulmonary infections in cystic fibrosis patients. Such  
CC infections are often resistant to the antibiotics normally used to treat  
CC pulmonary infections. Sequences AAB11976-B11984 represent specifically  
CC claimed histatin-related peptides for use in the method of the invention

XX SQ Sequence 12 AA;  
Query Match 52.9%; Score 27; DB 3; Length 12;  
Best Local Similarity 62.5%; Pred. No. 3.6e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 2 FGYNKSKF 9  
| | | | |  
5 FGYNKSKF 12  
DB  
RESULT 14  
AAW33942  
ID AAW33942 standard; peptide; 14 AA.  
XX AC AAW33942;  
XX DT 28-MAY-1998 (first entry)  
XX DE Beta1-adrenergic receptor antagonist.  
XX KW Antagonist; integral membrane protein; inhibitor; transmembrane domain;  
XX KM therapy; psychotic disorder; Huntington's disease; Parkinson's disease;  
XX KM post-myocardial infarction; HIV infection; cell proliferation disorder;  
XX KM peptic ulcer; glaucoma; asthma; renal disease; autoimmune disease;  
XX KM antibacterial; beta1-adrenergic receptor.  
XX OS Homo sapiens.  
XX PN WO9735881-A2.  
XX PD 02-OCT-1997.  
XX PF 26-MAR-1997; 97WO-CA000203.  
XX PR 27-MAR-1996; 96US-0014306P.  
XX PR 25-JUN-1996; 96US-00670119.  
XX PR 20-AUG-1996; 96US-0024240P.  
XX PA (NGGY/) NG G Y K.  
XX PA (SEEM/) SEEMAN P.  
XX PA (GEOR/) GEORGE S. R.  
XX PA (ODOW/) O'DOWD B. F.  
XX PI Ng GYK, Seeman P, George SR, Odowd BF;  
XX DR WPI; 1997-489566/45.  
XX PT Inhibitor of integral membrane protein - used to treat e.g.  
XX PT schizophrenia, hypertension, viral infection, cancer etc.  
XX PS Claim 17; Page 94; 127pp; English.  
XX  
CC This sequence is a beta1-adrenergic receptor antagonist, and is an  
CC antagonist of the invention. The antagonists (A) are for inhibiting the  
CC function of a prokaryotic or eukaryotic integral membrane protein (IMP)  
CC having at least one transmembrane domain (TMD), comprises a peptide  
CC including at least 4 consecutive amino acids (aa) from the sequence of  
CC the TMD. (A) are used to treat or prevent disorders in mammals that  
CC involve disturbances of IMP, and the same effect is achieved by inserting  
CC a nucleic acid encoding (A) into the cells of the mammal. Specified  
CC conditions that can be treated are schizophrenia, psychotic disorders,  
CC Huntington's disease, Tourette's syndrome, hypertension, post-myocardial  
CC infarction, tachyarrhythmia, human immunodeficiency virus infection,  
CC AIDS, cell proliferation (cancer, psoriasis or hyperkeratosis), and drug  
CC abuse. (A) can also be used to treat peptic ulcer, glaucoma, asthma,  
CC renal disease, Parkinson's disease, congestive heart failure, migraine,  
CC depression, obesity, diabetic neuropathy/retinopathy, autoimmune  
CC diseases, graft rejection etc. (A) can be used as diuretics and  
CC antibacterials. (A) may also be used to determine function of orphan  
CC receptors and, when attached to a marker, for tissue imaging to  
CC localise/quantify specific receptors. The transgenic animals are used to

CC test efficacy/toxicity of (A) and as models of diseases. (A) are very  
CC specific and selective, against the IMP from which they are derived, so  
CC should have few side effects  
XX  
SQ Sequence 14 AA;

Query Match 52.9%; Score 27; DB 2; Length 14;  
Best Local Similarity 71.4%; Pred. No. 4.3e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GYKSKF 9  
DB 6 GYNSAF 12

RESULT 15  
AAW68100  
ID AAW68100 standard; protein; 14 AA.

XX AAW68100;

DT 27-OCT-1998 (first entry)

DE Chlamydomonas reinhardtii RB47 binding protein peptide fragment.

KW RB47; activator; mRNA binding protein; psbA; chloroplast; recombinant;  
KM regulated production; protein synthesis; plant propagation.

OS Chlamydomonas reinhardtii.

XX WO9831823-A1.

PD 23-JUL-1998.

PF 16-JAN-1998; 98WO-US000840.

PR 17-JAN-1997; 97US-0035955P.

PR 12-DEC-1997; 97US-0069400P.

PA (SCRI ) SCRIPPS RES INST.

PI Mayfield S;

DR WPI; 1998-427562/36.

PT New isolated RB47 and RBE0 genes - used for, e.g. regulated expression of  
PT desired recombinant molecule in prokaryote and eukaryote, particularly  
PT plant cells.

PS Example 1; Page 58; 109pp; English.

CC The sequence is that of a fragment of the RB47 mRNA binding protein which  
CC was used in the isolation of the coding region of the complete gene

SQ Sequence 14 AA;

Query Match 52.9%; Score 27; DB 2; Length 14;  
Best Local Similarity 62.5%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GFGYKNSK 8  
DB 1 GFGFINFK 8

RESULT 16  
AAW16616  
ID AAW16616 standard; peptide; 11 AA.

XX AAW16616;

DT 19-DEC-1997 (first entry)

DE Phosphoinositide-3 kinase p110alpha conserved motif.  
XX  
KW Phosphoinositide 3 kinase; PI-3 kinase; wortmannin.

OS Synthetic.

XX WO9715658-A1.

PD 01-MAY-1997.

PF 28-OCT-1996; 96WO-GB002614.

PR 26-OCT-1995; 95GB-00021987.

PA (LUDW-) LUDWIG INST CANCER RES.

PI Wymann MP, Bulgarelli-Vela G, Panayotou G, Vanhaesebroeck B;  
PI Zvelebil MJ, Waterfield MD;

DR WPI; 1997-259013/23.

PT Phospho:inositide 3 kinase wortmannin interaction site - to identify and  
PT design ligands which regulate phospho:inositide 3 kinase activity.

PS Disclosure; Page 32; 71pp; English.

XX A novel interaction site has been discovered on phosphoinositide 3 (PI-3)  
CC kinase, or a homologue or analogue. The interaction site modulates the  
CC activity of PI-3 kinase when exposed to a modulator, and has a molecular  
CC shape adapted to interact with at least a part of the modulator so as to  
CC modulate PI-3 kinase activity. The present sequence represents a  
CC conserved motif (resembling K(X)NKKK where n=3-7) in PI-3 kinase  
CC p110alpha, that was found to bind phosphatidylinositol in gelsolin and so  
CC might constitute a binding site for the 4,5-phosphates of the lipid. The  
CC activity of PI-3 kinase can be regulated by altering, e.g. substituting a  
CC different amino acid or deleting any of the features of the site. The  
CC site may be used to identify or design novel ligands which regulate the  
CC activity of PI-3 kinase by generating a molecular model of the wortmannin  
CC inhibition site of PI-3 kinase, identifying or designing ligands which  
CC interact with at least part of the site and optionally contacting the  
CC putative ligand with PI-3 kinase and monitoring PI-3 kinase activity

XX SQ Sequence 11 AA;

Query Match 51.0%; Score 26; DB 2; Length 11;  
Best Local Similarity 57.1%; Pred. No. 5.1e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 FGYKNSK 8  
DB 5 FGYKRER 11

RESULT 17  
AAO22420  
ID AAO22420 standard; peptide; 12 AA.

XX AAO22420;

DT 11-OCT-2002 (first entry)

DE Protease cleavage site related peptide SEQ ID No 86.

XX Cytostatic; antiinflammatory; antibacterial; matrix metalloproteinase;  
KW protease cleavage site motif; enzyme; proteolytic enzyme; pathogenesis;  
KW B. anthracis; pla; YopJ protease; Yersinia; smallpox H1b metalloprotease;  
KW cathepsin family protease; TACE; calpain; caspase; BACE; beta-secretase;  
KW tumour necrosis factor-alpha converting enzyme; blood clotting cascade;  
KW beta-site amyloid precursor protein cleaving enzyme; presenilin; furin;  
KW membrane-type serine protease; proprotein convertase; protease inhibitor;  
KW proteasome; pathogenic infection; cancer; inflammatory disease.

XX Bos taurus.

XX WO200238796-A2.  
 PN 16-MAY-2002.  
 XX  
 XX 08-NOV-2001; 2001WO-US046777.  
 PF  
 XX 08-NOV-2000; 2000US-0246815P.  
 PR  
 XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
 PA  
 XX Turk BE, Cantley LC;  
 PI  
 XX WPI; 2002-519316/55.  
 DR  
 XX  
 XX Rapid determination of protease cleavage site motifs using a mixture-  
 PT based oriented peptide library.  
 PS  
 XX Example 8; Page 52; 126pp; English.  
 PS  
 CC The invention relates to a method for determining an amino acid sequence  
 CC motif for a cleavage site of a protease. The method comprises contacting  
 CC the protease with a peptide library containing degenerate residues which  
 CC allow for cleavage of a substrate by the protease, allowing the protease  
 CC to cleave peptides within the degenerate peptide library having a  
 CC cleavage site for the protease to form a population of cleaved peptides,  
 CC and determining an amino acid sequence motif for the cleavage site of the  
 CC protease. The protease of the method is a matrix metalloproteinase, or a  
 CC proteolytic enzyme that mediates the pathogenesis of a pathogen. The  
 CC protease is a lethal factor of B. anthracis, pla and YopJ proteases of  
 CC Yersinia, and the smallpox H1L metalloprotease. The protease of the  
 CC invention is selected from a protease of pathogenic organisms, cathepsin  
 CC family protease, tumour necrosis factor-alpha converting enzyme (TACE),  
 CC calpains, caspases, beta-site amyloid precursor protein cleaving enzyme  
 CC (BACE, beta-secretase), presenilins, membrane-type serine proteases,  
 CC furin and other proprotein convertases, proteasome components and  
 CC proteases affecting the blood clotting cascade. The protease inhibitors  
 CC of the invention are useful to treat diseases, including pathogenic  
 CC infections, cancer, and inflammatory diseases. This sequence represents a  
 CC peptide sequence relating to the protease cleavage site motifs of the  
 CC invention  
 CC  
 XX  
 SQ Sequence 12 AA;  
 Query Match 51.0%; Score 26; DB 5; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 5.5e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 FGYKNSX 8  
 DB 5 FGYKRER 11  
 RESULT 18  
 AAM97164  
 ID AAM97164 standard; peptide; 14 AA.  
 AC  
 XX AAM97164;  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE Human peptide #439 encoded by a SNP oligonucleotide.  
 XX  
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cyrostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 OS Homo sapiens.

XX WO200147944-A2.  
 PN 05-JUL-2001.  
 PD  
 XX  
 XX 28-DEC-2000; 2000WO-US035498.  
 PF  
 XX 28-DEC-1999; 99US-0173419P.  
 PR 27-DEC-2000; 2000US-00173419.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX Shimkets RA, Leach M;  
 PI  
 XX WPI; 2001-465210/50.  
 DR  
 XX  
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
 PT autoimmune diseases and infections.  
 PS  
 XX Disclosure; Page 3764; 4143pp; English.  
 PS  
 CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the proteins listed above. Disorders that may  
 CC be prevented, diagnosed and/or treated include multifactorial diseases  
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus  
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 CC system and an infection of pathogenic organisms  
 CC  
 XX  
 SQ Sequence 14 AA;  
 Query Match 51.0%; Score 26; DB 4; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 6.5e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GFGYKNSKP 9  
 DB 3 GAEPDNNKF 11  
 RESULT 19  
 AAM99539  
 ID AAM99539 standard; peptide; 14 AA.  
 AC  
 XX AAM99539;  
 DT 07-DEC-2001 (first entry)  
 XX  
 DE Vaccine related MHC ligand peptide SEQ ID NO:642.  
 XX  
 KW Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;  
 KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;  
 KW bactericidal; antiparasitic; fungicidal; cyrostatic; medicine;  
 KW pharmaceutical; immune disorder; immune deficiency; autoimmune;  
 KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;  
 KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;  
 KW human immunodeficiency virus.  
 XX  
 OS Clostridium tetani.  
 XX  
 PN WO200170772-A2.  
 XX 27-SEP-2001.



XX 22-MAR-2001; 2001WO-FR000872.  
 PF  
 XX  
 PR 23-MAR-2000; 2000FR-00003711.  
 XX  
 PA (FABR ) FABRE MEDICAMENT SA PIERRE.  
 XX  
 PI Klingner-Hamouir C, Corvaia N, Beck A, Goetsch L;  
 XX  
 DR WPI; 2001-611470/70.  
 XX  
 PT Stabilized pharmaceutical containing N-terminal glutamic acid or  
 PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt  
 PT with strong acid.  
 XX  
 PS Claim 9; Page 140; 149pp; French.  
 XX  
 CC The present invention describes a pharmaceutical compound (I) that  
 CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in  
 CC the form of an addition salt with a strong, physiologically acceptable  
 CC acid (II). Also described are: (a) a pharmaceutical composition  
 CC containing at least one (I); (b) a vaccine containing at least one (I)  
 CC where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a  
 CC method for in vitro diagnosis of diseases associated with the presence of  
 CC (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process  
 CC for preparing (I). (I) has immunomodulator, endocrine, antiallergic,  
 CC neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and  
 CC cytostatic activities. (I) are useful, in human or veterinary medicine,  
 CC in pharmaceutical compositions (for treating immune disorders, e.g.  
 CC immune deficiency, autoimmune states, hypersensitivity, allergy, graft  
 CC rejection, infection, hormonal disorders and central nervous system  
 CC diseases), also, where (I) is a MHC ligand (Ia), in vaccines for  
 CC treatment or prevention of: (i) viral, bacterial, parasitic or fungal  
 CC infections; or (ii) of cancers. A particular application is in anti-  
 CC melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases  
 CC associated with interactions between MHC and (I), e.g. melanoma and human  
 CC immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides  
 CC which can be used in pharmaceutical compounds from the present invention  
 XX  
 SQ Sequence 14 AA;  
 QY 5 KNSKF 9  
 Db 5 KNSKF 9  
 Query Match 51.0%; Score 26; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 20  
 ADB71196  
 ID ADB71196 standard; peptide; 14 AA.  
 XX  
 AC ADB71196;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Human modified protein C peptide SEQ ID NO:42.  
 XX  
 KW variant blood coagulation component; anticoagulant; protein C;  
 KW activated protein C; blood; thrombolytic; anticoagulant;  
 KW coagulation disorder; thrombosis; mutant; variant.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO2003073980-A2.  
 XX  
 PD 12-SEP-2003.  
 XX  
 PF 28-FEB-2003; 2003WO-SB000331.  
 XX

PR 01-MAR-2002; 2002US-0360181P.  
 PR 06-AUG-2002; 2002US-0401042P.  
 XX  
 PA (TACT-) TAC THROMBOSIS & COAGULATION AB.  
 XX  
 PI Dahlbaeck B;  
 XX  
 DR WPI; 2003-722004/68.  
 XX  
 PT New variant blood coagulation component substantially homologous to  
 PT protein C or activated protein C useful for preparing a composition for  
 PT treating or preventing coagulation disorders.  
 XX  
 PS Example 1; Page 46; 113pp; English.  
 XX  
 CC The present invention describes a variant blood coagulation component (I)  
 CC which is substantially homologous in amino acid sequence to a wild-type  
 CC anticoagulant protein in the protein C-anticoagulant system selected from  
 CC protein C (PC) and activated protein C (APC). (I) exhibits enhanced  
 CC anticoagulant activity compared to the wild-type blood component, and  
 CC comprises at least one amino acid sequence modification in its 45 N-  
 CC terminal amino acids (the Gla-domain), and at least one amino acid  
 CC sequence modification in a region corresponding to the serine-protease  
 CC (SP) domain of the wild-type protein. Also described: (1) a DNA segment  
 CC comprising a nucleotide sequence encoding (I); (2) a DNA vector  
 CC (especially an expression vector) comprising the DNA segment of (1); (3)  
 CC a microorganism or (preferably an) animal host cell stably transfected  
 CC with the vector of (2); (4) producing the DNA segment coding for the  
 CC variant blood coagulation component by introducing mutations into the  
 CC wild-type DNA and replicating the modified DNA produced; (5) producing  
 CC (I) from a culture of the transfected host cell; (6) a diagnostic test  
 CC system, especially a kit, for assaying components participating in the  
 CC protein C-anticoagulant system of blood, comprising (I); and (7)  
 CC inhibiting coagulation in a patient by administering a composition  
 CC containing (I). (I) has thrombolytic and anticoagulant activities. The  
 CC variant blood coagulation component (I) is useful in the manufacture of a  
 CC medicament for treating or preventing coagulation disorders, such as  
 CC thrombosis. The medicament is especially suitable for treating a patient  
 CC with APC resistance. The assay system is useful for assaying components  
 CC participating in the protein C-anticoagulant system of blood. The  
 CC variants exhibit increased anticoagulant activity compared to the wild-  
 CC type protein. The present sequence represents a human modified protein C  
 CC peptide, which is given in the exemplification of the present invention.  
 XX  
 SQ Sequence 14 AA;  
 QY 1 GFGYKNSK 8  
 Db 3 GWGYHSSR 10  
 Query Match 51.0%; Score 26; DB 7; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 6.5e+02;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 RESULT 21  
 AAM99439  
 ID AAM99439 standard; peptide; 9 AA.  
 XX  
 AC AAM99439;  
 XX  
 DT 07-DEC-2001 (first entry)  
 XX  
 DE Vaccine related MHC ligand peptide SEQ ID NO:542.  
 XX  
 KW Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;  
 KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;  
 KW bactericidal; antiparasitic; fungicidal; cytostatic; medicine;  
 KW pharmaceutical; immune disorder; immune deficiency; autoimmune;  
 KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;  
 KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;  
 KW human immunodeficiency virus.  
 XX



OS Homo sapiens.  
XX WO200170772-A2.  
PN 27-SEP-2001.  
XX 22-MAR-2001; 2001WO-FR000872.  
PF 23-MAR-2000; 2000FR-00003711.  
XX (FABR ) FABRE MEDICAMENT SA PIERRE.  
PA Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;  
XX MPI; 2001-611470/70.  
XX Stabilized pharmaceutical containing N-terminal glutamic acid or  
PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt  
PT with strong acid.  
XX  
PS Claim 9; Page 123; 149pp; French.  
XX  
XX The present invention describes a pharmaceutical compound (I) that  
CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in  
CC the form of an addition salt with a strong, physiologically acceptable  
CC acid (II). Also described are: (a) a pharmaceutical composition  
CC containing at least one (I); (b) a vaccine containing at least one (I)  
CC where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a  
CC method for in vitro diagnosis of diseases associated with the presence of  
CC (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process  
CC for preparing (I). (I) has immunomodulator, endocrine, antiallergic, and  
CC neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and  
CC cyostatic activities. (I) are useful, in human or veterinary medicine,  
CC in pharmaceutical compositions (for treating immune disorders, e.g.  
CC immune deficiency, autoimmune states, hypersensitivity, allergy, graft  
CC rejection, infection, hormonal disorders and central nervous system  
CC diseases), also, where (I) is a MHC ligand (Ia), in vaccines for  
CC treatment or prevention of: (i) viral, bacterial, parasitic or fungal  
CC infections; or (ii) of cancers. A particular application is in anti-  
CC melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases  
CC associated with interactions between MHC and (I), e.g. melanoma and human  
CC immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides  
CC which can be used in pharmaceutical compounds from the present invention  
XX  
SQ Sequence 9 AA;  
  
Query Match 49.0%; Score 25; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
  
QY 1 GFGY 4  
|||  
Db 4 GFGY 7  
  
RESULT 22  
ID AAM99577 standard; peptide; 9 AA.  
XX AAM99577;  
AC AAM99577;  
XX  
DT 07-DEC-2001 (First entry)  
XX  
DE Vaccine related MHC ligand peptide SEQ ID NO:680.  
XX  
KW Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;  
KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;  
KW bactericidal; antiparasitic; fungicidal; cyostatic; medicine;  
KW pharmaceutical; immune disorder; immune deficiency; autoimmune;  
KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;  
KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;  
KW human immunodeficiency virus.  
XX

|                         |   |
|-------------------------|---|
| OS                      | Homo sapiens.   |
| XX                      |   |
| FN                      | WO200170772-A2.   |
| PD                      |   |
| XX                      | 27-SEP-2001.  |
| PF                      |   |
| XX                      | 22-MAR-2001; 2001WO-FR000872.   |
| PR                      |   |
| XX                      | 23-MAR-2000; 2000FR-00003711.   |
| PA                      | (FABR ) FABRE MEDICAMENT SA PIERRE.                                       |
| PI                      | Klingner-Hamour C, Corvaia N, Beck A, Goetsch L;                          |
| XX                      |   |
| DR                      | WPI; 2001-611470/70.  |
| XX                      |   |
| PT                      | Stabilized pharmaceutical containing N-terminal glutamic acid or          |
| PT                      | glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt     |
| PT                      | with strong acid.   |
| XX                      |   |
| PS                      | Claim 9; Page 146; 149pp; French.   |
| XX                      |   |
| CC                      | The present invention describes a pharmaceutical compound (I) that        |
| CC                      | contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in  |
| CC                      | the form of an addition salt with a strong, physiologically acceptable    |
| CC                      | acid (II). Also described are: (a) a pharmaceutical composition           |
| CC                      | containing at least one (I); (b) a vaccine containing at least one (I)    |
| CC                      | where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a |
| CC                      | method for in vitro diagnosis of diseases associated with the presence of |
| CC                      | (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process    |
| CC                      | for preparing (I). (I) has immunomodulator, endocrine, antiallergic,      |
| CC                      | neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and   |
| CC                      | cytostatic activities. (I) are useful, in human or veterinary medicine,   |
| CC                      | in pharmaceutical compositions (for treating immune disorders, e.g.       |
| CC                      | immune deficiency, autoimmune states, hypersensitivity, allergy, graft    |
| CC                      | rejection, infection, hormonal disorders and central nervous system       |
| CC                      | diseases), also, where (I) is a MHC ligand (Ia), in vaccines for          |
| CC                      | treatment or prevention of: (i) viral, bacterial, parasitic or fungal     |
| CC                      | infections; or (ii) of cancers. A particular application is in anti-      |
| CC                      | melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases |
| CC                      | associated with interactions between MHC and (I), e.g. melanoma and human |
| CC                      | immunodeficiency virus infection. AAM98898 to AAM9592 represent peptides  |
| CC                      | which can be used in pharmaceutical compounds from the present invention  |
| XX                      |   |
| SQ                      | Sequence 9 AA;  |
|                         |   |
| Query Match             | 49.0%; Score 25; DB 4; Length 9;  |
| Best Local Similarity   | 100.0%; Pred. No. 1.4e+06;  |
| Matches 4; Conservative | 0; Mismatches 0; Indels 0;  |
| Gy                      | 1 GFGY 4<br>  |
| Db                      | 6 GFGY 9  |
|                         |   |
| RESULT 23               |   |
| ID                      | AAM28520 standard; peptide; 10 AA.  |
| XX                      |   |
| AC                      | AAW28520;   |
| XX                      |   |
| DT                      | 11-JAN-1998 (first entry)   |
| XX                      |   |
| DE                      | Human Herpes VI sequence.   |
| XX                      |   |
| KM                      | Biosensor; capture; ligand; ion; electron; channel; current;              |
| KM                      | Herpes virus.   |
| XX                      |   |
| OS                      | Synthetic.  |
| XX                      |   |
| PN                      | AT9501943-A.  |
| XX                      |   |
| PD                      | 15-APR-1997   |

```
XX 28-NOV-1995; 95AT-00001943.
XX
XX 28-NOV-1995; 95AT-00001943.
XX
XX (SCHA/) SCHALKHAMMER T.
XX (PITT/) PITTMER F.
XX
XX WPI; 1997-272445/25.
XX
XX Bio:sensor for nucleic acid determination - with capture ligands
XX immobilised in ion channels in membrane.
XX
XX Example 12; Page 9; 17pp; German.
XX
XX Example 12 describes the prodn. of a Herpes virus biosensor where the
XX capture ligands (oligonucleotides) are based on the sequences given in
XX AAW28515-W28526. The biosensor is useful for determining DNA or RNA
XX concentrations by a method comprising measuring changes in ion and/or
XX electron current induced by hybridisation in the channels
XX
XX Sequence 10 AA;
XX
SQ
Query Match 49.0%; Score 25; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 7e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GFGYKNS 7
DB 3 GIGYKGA 9

RESULT 24
AAW63824
ID AAW63824 standard; peptide; 10 AA.
XX
XX AAW63824;
XX
XX 28-SEP-1998 (first entry)
XX
XX Human Mab #117-10C heavy chain CDR3 peptide fragment.
XX
XX Interleukin-18: IL-18; human; treatment; autoimmune disease; Mab;
XX immunosuppressant; inhibitor; receptor protein; detection; heavy chain;
XX monoclonal antibody; Mab; complementarity determining region; CDR3.
XX
XX Homo sapiens.
XX
XX EP850952-A1.
XX
XX 01-JUL-1998.
XX
XX 23-DEC-1997; 97EP-00310555.
XX
XX 26-DEC-1996; 96JP-00356426.
XX
XX 21-FEB-1997; 97JP-00052526.
XX
XX 06-JUN-1997; 97JP-00163490.
XX
XX 28-JUL-1997; 97JP-00215490.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Torigoe K, Ushio S, Kunikata T, Kurimoto M;
XX
XX WPI; 1998-335317/30.
XX
XX New interleukin-18 receptor protein - used to inhibit interleukin-18, to
XX treat autoimmune disease and as immunosuppressant to treat e.g. graft
XX rejection, insulin-resistant diabetes and ulcerative colitis.
XX
XX Claim 14; Page 20; 35pp; English.
XX
XX This sequence represents the human monoclonal antibody (Mab) #117-10C
XX heavy chain complementarity determining region, CDR3 which is used in a
```

```
CC method involved in neutralising IL-18 or to treat autoimmune diseases or
CC as an immunosuppressant using anti-IL-18 antibodies which can inhibit IL-
CC 18. Such antibodies can also be used to detect the IL-18 receptor protein
CC (labelled with an enzyme or a radioactive or fluorescent substance). The
CC protein is used to treat e.g. graft rejection, pernicious anaemia,
CC atrophic gastritis, insulin-resistant diabetes, Wegener granulomatosis,
CC discoid lupus erythematosus, ulcerative colitis, cold-agglutinin-relating
CC diseases, Goodpasture's syndrome, primary biliary cirrhosis, sympathetic
CC ophthalmitis, hyperthyroidism, juvenile onset type diabetes, Sjogren
CC syndrome, autoimmune hepatitis, autoimmune haemolytic anaemia, myasthenia
CC gravis, systemic scleroderma, systemic lupus erythematosus, polypleptic
CC cold haemaglobinuria, polymyositis, periarthritis nodosa, multiple
CC sclerosis, Addison's disease, purpura haemorrhagica, Basedow's disease,
CC leukopaenia, Behcet's disease, climacterium praecox, rheumatoid
CC arthritis, rheumatopyra, chronic thyroiditis, Hodgkin's disease, HIV,
CC asthma, atopic dermatitis, allergic nasitis, pollinosis, apitoxin-
CC allergy and septic shock resulting from production or administration of
CC excessive gamma interferon (IFN-gamma)
XX
XX Sequence 10 AA;
XX
SQ
Query Match 49.0%; Score 25; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFGY 4
DB 7 GFGY 10

RESULT 25
AAB46262
ID AAB46262 standard; peptide; 10 AA.
XX
XX AAB46262;
XX
XX 04-APR-2001 (first entry)
XX
XX HPV type 16 cytotoxic T-cell epitope SEQ ID NO 17.
XX
XX Cytotoxic T cell; epitope; L1 protein; antiviral; antitumor; antigen;
XX vaccine; tumor; protective immune response.
XX
XX Human papillomavirus.
XX
XX DE19925235-A1.
XX
XX 07-DEC-2000.
XX
XX 01-JUN-1999; 99DE-01025235.
XX
XX 01-JUN-1999; 99DE-01025235.
XX
XX (MEDI-) MEDIGENE AG.
XX (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX Schaefer K, Faath S, Jochmus I, Nieland J, Osen W;
XX
XX WPI; 2001-062580/08.
XX
XX New T cell epitopes from the papilloma virus L1 protein, useful for
XX detecting or inducing an immune response, e.g. in vaccines.
XX
XX Example 4; Page 18; 26pp; German.
XX
XX This invention describes novel T cell epitopes (A) of the human papilloma
XX virus L1 protein. The invention also describes (a) compounds (I)
XX containing an (A) provided it is not a natural L1 protein nor an
XX exclusively N- or C-terminal deletion variant of natural L1; (b) nucleic
XX acid (II) that encodes (A) or (I); (c) vector, particularly an expression
XX vector, that contains (II); (d) cells that contain, and preferably
XX present, (A); (e) complex of (A) or (I) with at least one additional
XX molecule (III); in vitro detection of T cell activation by a compound
```

CC containing at least one (A); (f) preparing cells of (d); and (g) test  
CC system for in vitro detection of T cells. The products of the invention  
CC have antiviral and antitumor activity. (A), also compounds or complexes  
CC containing it or nucleic acid or vectors encoding it, is used for  
CC detection of an immune response, particularly detecting Li-specific  
CC cytotoxic T cells or to determine the Li protein-specific antigenicity of  
CC compounds and complexes that contain (A), and for inducing a protective  
CC immune response against papilloma virus and related tumors, particularly  
CC as vaccines  
XX  
SQ Sequence 10 AA;

Query Match 49.0%; Score 25; DB 4; Length 10;  
Best Local Similarity 66.7%; Pred. No. 7e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YKNSKF 9  
| | | | |  
Db 1 YKNTNF 6

RESULT 26  
ABR91208  
ID ABR91208 standard; peptide; 10 AA.

AC ABR91208;  
XX  
DT 10-SEP-2003 (first entry)

DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:42.

KM Phlebotomus papatasi; salivary polypeptide; antigenic; immunogenic;  
KW protozoacide; immunostimulant; vaccine; immune response; Leishmaniasis.

OS Phlebotomus papatasi.  
OS Synthetic.

PN WO2002102324-A2.

PD 27-DEC-2002.

PF 18-JUN-2002; 2002WO-US019663.

PR 19-JUN-2001; 2001US-0299391P.

PA (USSH.) US DEPT HEALTH & HUMAN SERVICES.

PI Valenzuela JG, Belkaid Y, Kamhawi S, Sacks D, Ribeiro JMC;  
XX WPI; 2003-157000/15.

PT Novel isolated salivary polypeptide of Phlebotomus papatasi, useful for  
PT producing an immune response in a subject or for preventing Leishmaniasis  
PT in a subject.

PS Claim 10; Page 78; 279pp; English.

XX The present invention describes an isolated salivary polypeptide (I), of  
CC Phlebotomus papatasi. Also described: (1) an isolated nucleic acid (II)  
CC encoding (I); (2) an isolated fragment (Iir) of (II), where the fragment  
CC encodes the polypeptide fragment specific for a polypeptide such as  
CC Phlebotomus papatasi salivary polypeptide (PSP) 12, PPS14, PPS15,  
CC PPS30, PPS32, PPS36, PPS42 or PPS44; (3) an isolated antigenic or  
CC immunogenic fragment (IV) of (I); (4) a nucleic acid (V) that hybridises  
CC under stringent conditions to (II); (5) a vector (VI) comprising (II) or  
CC (Iir); and (6) a composition (VII) comprising (I) or its fragment, (IV)  
CC or (VI), and a pharmaceutically acceptable carrier. (I) has protozoacide  
CC and immunostimulant activities, and can be used in vaccines. (VII) is  
CC useful for producing an immune response in a subject or for preventing  
CC Leishmaniasis in a subject. (II) is also useful for preventing  
CC Leishmaniasis in a subject. (VII) is useful as a vaccine. ACC79987 to  
CC ACC79999 and ABR91176 to ABR92046 represent sequences used in the  
CC exemplification of the present invention

XX  
SQ Sequence 10 AA;

Query Match 49.0%; Score 25; DB 6; Length 10;  
Best Local Similarity 37.5%; Pred. No. 7e+02;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 FGYKNSKF 9  
: | : | : |  
Db 3 YGFANDKY 10

RESULT 27  
AAB81464  
ID AAB81464 standard; peptide; 12 AA.

AC AAB81464;

DT 18-JUN-2001 (first entry)

DE Synthetic peptide, SEQ ID NO: 10.

KM Peptidomimetic; beta-hairpin loop mimetic; binding motif identification;  
KW drug design; protein target identification.

OS Synthetic.

PN WO200116161-A1.

PD 08-MAR-2001.

PF 30-AUG-1999; 99WO-EP006369.

PR 30-AUG-1999; 99WO-EP006369.

PA (POLY-) POLYPHOR AG.

PI Robinson JA, Obrecht D;

DR WPI; 2001-273332/28.

PT Method for manufacturing template-fixed beta-hairpin loop mimetics,  
PT useful for designing small peptidomimetic drug candidates, involves  
PT process based on mixed solid and solution phase synthetic strategy.

PS Claim 7; Page 77; 83pp; English.

XX The present sequence is part of a template-fixed, beta-hairpin loop  
CC peptidomimetic which may be manufactured by the process disclosed in this  
CC invention. The process is based on a mixed solid and solution phase  
CC synthetic strategy. The method is useful for determining key amino acids  
CC and motifs important for binding large surface and flat protein  
CC interfaces in their sequential and/or spatial arrangement. This  
CC information can ultimately be used for the design of small peptidomimetic  
CC drug candidates. The peptidomimetics may be used to probe large surface  
CC protein-protein interactions and to find protein targets  
XX

SQ Sequence 12 AA;

Query Match 49.0%; Score 25; DB 4; Length 12;  
Best Local Similarity 50.0%; Pred. No. 8.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYKNSKF 9  
: | | | : | : |  
Db 4 YGVKNSFW 11

RESULT 28  
AAB81463  
ID AAB81463 standard; peptide; 12 AA.

AC AAB81463;

XX 18-JUN-2001 (first entry)  
XX  
XX Synthetic peptide, SEQ ID NO: 9.  
DE  
XX Peptidomimetic; beta-hairpin loop mimetic; binding motif identification;  
KW drug design; protein target identification.  
XX  
XX Synthetic.  
OS  
XX WO200116161-A1.  
PN  
XX 08-MAR-2001.  
PD  
XX 30-AUG-1999; 99WO-EP006369.  
PF  
XX 30-AUG-1999; 99WO-EP006369.  
PR  
XX (POLY-) POLYPHOR AG.  
PA  
XX Robinson JA, Obrecht D;  
PI  
XX WPI; 2001-273332/28.  
DR  
XX Method for manufacturing template-fixed beta-hairpin loop mimetics,  
PT useful for designing small peptidomimetic drug candidates, involves  
PT process based on mixed solid and solution phase synthetic strategy.  
XX  
XX Claim 7; Page 77; 83pp; English.  
PS  
XX The present sequence is part of a template-fixed, beta-hairpin loop  
CC peptidomimetic which may be manufactured by the process disclosed in this  
CC invention. The process is based on a mixed solid and solution phase  
CC synthetic strategy. The method is useful for determining key amino acids  
CC and motifs important for binding large surface and flat protein  
CC interfaces in their sequential and/or spatial arrangement. This  
CC information can ultimately be used for the design of small peptidomimetic  
CC drug candidates. The peptidomimetics may be used to probe large surface  
CC protein-protein interactions and to find protein targets  
CC  
SQ Sequence 12 AA;  
Query Match 49.0%; Score 25; DB 4; Length 12;  
Best Local Similarity 50.0%; Pred. No. 8.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 2 FGYNKSF 9  
Db 4 YGVNSENW 11  
RESULT 29  
ABR74314  
ID ABR74314 standard; peptide; 12 AA.  
AC ABR74314;  
XX 18-APR-2002 (first entry)  
DT  
XX Simple nuclear localisation signal peptide SEQ ID NO:78.  
DE  
XX Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;  
KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;  
KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
KW breast carcinoma; prostate carcinoma.  
XX  
XX Synthetic.  
OS  
XX WO200193836-A2.  
PN  
XX 13-DEC-2001.  
PD  
XX 08-JUN-2001; 2001WO-US018657.  
PF

XX 09-JUN-2000; 2000US-0210925P.  
PR  
XX (BOUL/) BOULIKAS T.  
PA  
XX Boulikas T;  
PI  
XX WPI; 2002-164295/21.  
DR  
XX Encapsulation of plasmid DNA (lipogenes) and therapeutic agents with  
PT nuclear localisation signal/fusogenic peptide conjugates into targeted  
PT liposome complexes.  
PT  
XX Claim 14; Page 57; 107pp; English.  
PS  
XX The present invention describes a method for producing micelles with  
CC entrapped therapeutic agents. The method comprises: (1) combining  
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %  
CC of the negatively charged atoms are neutralised by positive charges on  
CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-  
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing  
CC micelles with entrapped therapeutic agents. Also described is a method  
CC for delivering a therapeutic agent in vivo, comprising the administration  
CC of the micelle. ABR74256 to ABR74858 represent specifically claimed  
CC nuclear localisation signal (NLS) peptides for use in the method as the  
CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
CC and antitumour activities. The peptide-lipid-polynucleotide complexes  
CC produced are useful for inhibiting the progression of neoplastic  
CC diseases. The invention relates to the field of gene therapy and is  
CC directed toward methods for producing peptide-lipid-polynucleotide  
CC complexes suitable for delivery of polynucleotides. The encapsulated  
CC molecules display therapeutic efficacy in eradicating solid tumours  
CC including but not limited to breast carcinoma or prostate carcinoma.  
CC ABR74235 to ABR74255 are used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 12 AA;  
Query Match 49.0%; Score 25; DB 5; Length 12;  
Best Local Similarity 50.0%; Pred. No. 8.4e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GFYKNSK 8  
Db 2 GYGDNRKK 9  
RESULT 30  
AAE28582  
ID AAE28582 standard; peptide; 12 AA.  
AC AAE28582;  
XX 27-DEC-2002 (first entry)  
DT  
XX Desmodium uncinatum leucoanthocyanidin reductase (LAR) peptide #5.  
DE  
XX leucoanthocyanidin reductase; LAR; reductase-epimerase-dehydrogenase;  
KW RED; proanthocyanidin; pasture quality; legume; bloat-safe forage crop;  
KW disease resistance; pest resistance; enzyme.  
XX  
XX Desmodium uncinatum.  
OS  
XX Key Location/Qualifiers  
FH Misc-difference 1 /label= Leu, Ile  
FT Misc-difference 9 /label= Leu, Ile  
FT Misc-difference 10 /label= Leu, Ile  
FT Misc-difference 10 /label= Leu, Ile  
XX  
PN WO200266625-A1.

XX 29-AUG-2002.  
 PD 21-FEB-2002; 2002WO-AU000179.  
 XX 21-FEB-2001; 2001AU-00003241.  
 PF (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 XX (MEAT-) MEAT & LIVESTOCK AUSTRALIA LTD.  
 PA  
 XX  
 PI Tanner GJ, Ashton AR, Abrahams S, Watson JM, Larkin PJ;  
 PI Francki KT;  
 XX WPI; 2002-691619/74.  
 DR  
 XX New IAR polypeptide from the RED protein superfamily, useful for  
 PT regulating the biosynthesis and accumulation of proanthocyanidins in  
 PT plants, and modifying the pasture quality of legumes.  
 XX  
 PS Claim 6; Page 135; 175pp; English.  
 XX  
 CC The present invention relates to novel leucoanthocyanidin reductase (LAR)  
 CC proteins of reductase-epimerase-dehydrogenase (RED) protein superfamily  
 CC and polynucleotides encoding such proteins. LAR sequences are useful for  
 CC regulating the biosynthesis and accumulation of proanthocyanidins in  
 CC plants. They are useful for modifying the pasture quality of legumes, in  
 CC particular to produce bioat-safe forage crops or crops having enhanced  
 CC nutritional value, enhanced disease resistance or pest resistance or  
 CC enhanced malting qualities. The present sequence is Desmodium uncinatum  
 CC LAR peptide  
 XX  
 SQ Sequence 12 AA;  
 OY  
 DB 1 GFGY 4  
 2 GFGY 5  
 DB  
 Query Match 49.0%; Score 25; DB 5; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 31  
 AAW94978  
 ID AAW94978 standard; peptide; 13 AA.  
 XX  
 AC AAW94978;  
 DT 12-MAY-1999 (first entry)  
 XX  
 DE MHC binding peptide from myelin basic protein (MBP).  
 XX  
 KW Major histocompatibility class II; MHC; binding; vaccine; MBP;  
 KW autoimmune disease; myelin basic protein; HLA-DRB1\*0401.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9859244-A1.  
 PD 30-DEC-1998.  
 XX  
 PF 19-JUN-1998; 98WO-GB001801.  
 XX  
 PR 20-JUN-1997; 97GB-00012892.  
 XX  
 PA (ECLA-) ECLA GEN LTD.  
 XX  
 PI Fothergill J, Kemp G, Brooks T, Carr F;  
 XX WPI; 1999-105639/09.  
 DR  
 XX Identifying MHC binding peptides - by ascertaining the characteristics of  
 PT a MHC molecule binding groove and determining conformation scores of

PT pocket bound peptides.  
 XX  
 PS Example 4; Page 50; 64pp; English.  
 XX  
 CC The invention relates to a method for the prediction of the binding  
 CC affinity of a peptide to major histocompatibility (MHC) class II  
 CC molecules. The method comprises (a) ascertaining the characteristics of a  
 CC MHC molecule binding groove; (b) presenting a selected peptide to the MHC  
 CC molecule and ascertaining a first conformation score for each pocket  
 CC bound peptide side-chain; (c) amending the conformation of each pocket  
 CC bound peptide side-chain and ascertaining a second conformation score;  
 CC (d) repeating (c) with alternative conformations of each peptide pocket  
 CC bound side-chain; (e) choosing the highest conformation score for each  
 CC pocket bound peptide side-chain in each binding groove pockets; and (f)  
 CC combining the highest conformation score for each pocket and ascertaining  
 CC a binding score for the complete peptide. The invention also provides a  
 CC computer conditioned to receive information characterising a peptide  
 CC bound to the MHC molecule and to utilise the information to predict the  
 CC binding affinity of the peptide. The method can be used to identify  
 CC peptides in a protein which can bind to a given MHC molecule. Such  
 CC peptides can be used in the production of molecules for use in e.g.  
 CC vaccines, autoimmune diseases and diagnostics. Sequences AAW94957 to  
 CC AAW94981 represent peptides from myelin basic protein (MBP) that can bind  
 CC with MHC molecule HLA-DRB1\*0401  
 XX  
 SQ Sequence 13 AA;  
 OY  
 DB 1 GFGY 4  
 2 GFGY 5  
 DB  
 Query Match 49.0%; Score 25; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 32  
 AAB13279  
 ID AAB13279 standard; peptide; 13 AA.  
 XX  
 AC AAB13279;  
 DT 12-JAN-2001 (first entry)  
 XX  
 DE Caenorhabditis elegans conserved sequence #27.  
 XX  
 KW Caenorhabditis elegans; metabolic enzyme; AKT kinase; daf-18;  
 KW insulin signalling pathway; daf-2; age-1; insulin receptor; PI 3-kinase;  
 KW PKB kinase; PTEN lipid phosphatase; antidiabetic; anorectic; obesity;  
 KW diabetes.  
 XX  
 OS Caenorhabditis elegans.  
 XX  
 PN WO200033068-A1.  
 PD 08-JUN-2000.  
 XX  
 PF 02-DEC-1999; 99WO-US028529.  
 XX  
 PR 03-DEC-1998; 98US-00205658.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX  
 PI Ruvkun G, Ogg S;  
 XX WPI; 2000-423022/36.  
 DR  
 XX Diagnosing and treating obesity and impaired glucose tolerance using  
 PT modulators of daf-18 expression and/or activity.  
 XX  
 PS Disclosure; Page 171; 402pp; English.  
 XX  
 CC The present sequence is conserved protein region of a Caenorhabditis

CC elegans homologue of a key metabolic enzyme. A number of C. elegans genes  
CC have been identified as homologues of genes in the mammalian insulin  
CC signalling pathway. The C. elegans age-1 gene encodes a homologue of the  
CC mammalian PI 3-kinase whilst daf-2 encodes a homologue of the mammalian  
CC insulin receptor. The C. elegans AKT kinase and PKB kinase act downstream  
CC of daf-2 and age-1, just as their mammalian homologues act downstream of  
CC insulin signalling. The C. elegans PTEN lipid phosphatase homologue, DAF-  
CC 18, has been found to act upstream of AKT in the pathway. This discovery  
CC has enabled mammalian PTEN action to be mapped to the insulin signalling  
CC pathway. Conserved DAF motifs can be used to design probes to identify  
CC mammalian DAF homologues and thus to identify individuals with a  
CC predisposition toward the development of glucose intolerance conditions,  
CC such as obesity and diabetes

CC  
XX  
SQ Sequence 13 AA;

Query Match 49.0%; Score 25; DB 3; Length 13;  
Best Local Similarity 66.7%; Pred. No. 9.1e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GFGYKN 6  
|||:  
Db 2 GFGWKN 7

## RESULT 33

ADD44065  
ID ADD44065 standard; peptide; 13 AA.

AC ADD44065;

DT 15-JAN-2004 (first entry)

DE CPG2 peptide #85 with potential human MHC class II binding activity.

XX bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;

KW immunogenic; T-cell epitope; MHC class II binding ligand;

KW immunostimulant; enzyme therapy; immune response;

XX gene directed enzyme prodnug strategy; vaccine; enzyme; EC 3.4.17.11.

OS Pseudomonas sp. RS-16.

XX WO2003045426-A1.

XX 05-JUN-2003.

XX 27-NOV-2002; 2002WO-EP013351.

XX 29-NOV-2001; 2001EP-00128519.

XX 25-JAN-2002; 2002EP-00001778.

XX 13-SEP-2002; 2002EP-00020634.

XX (MERE ) MERCK PATENT GMBH.

XX Hellendoorn K, Baker M, Williams S, Carr FJ;

XX WPI; 2003-513617/48.

XX Claim 3; Page 13; 52pp; English.

CC The invention relates to a novel modified bacterial enzyme  
CC carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2  
CC proteins that are substantially non-immunogenic or less immunogenic than  
CC any non-modified CPG2 having essentially the same biological specificity  
CC when used in vivo, and comprising specific amino acid residues having  
CC alterations compared with the non-modified parochial enzyme. The  
CC alterations cause a reduction or an elimination of one or more of T-cell  
CC epitope sequences, which act in the parental enzyme as MHC class II  
CC binding ligands and stimulate T-cells. The modified CPG2 enzyme and the

CC CPG2 proteins have immunostimulant activity and may be used in enzyme  
CC therapy. The modified CPG2 enzyme may be used to induce an immune  
CC response in a human host, or as a therapeutic entity such as the gene  
CC directed enzyme prodnug strategy. The peptide is useful for the  
CC manufacture of a modified CPG2 enzyme having substantially no or less  
CC immunogenicity than any non-modified parental enzyme when used in vivo,  
CC and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.  
CC This sequence represents a CPG2 enzyme peptide with potential human MHC  
CC class II binding activity of the invention.

CC  
XX  
SQ Sequence 13 AA;

Query Match 49.0%; Score 25; DB 7; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFGY 4  
|||:  
Db 7 GFGY 10

## RESULT 34

ADD44039  
ID ADD44039 standard; peptide; 13 AA.

AC ADD44039;

DT 15-JAN-2004 (first entry)

DE CPG2 peptide #59 with potential human MHC class II binding activity.

XX bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;

KW immunogenic; T-cell epitope; MHC class II binding ligand;

KW immunostimulant; enzyme therapy; immune response;

XX gene directed enzyme prodnug strategy; vaccine; enzyme; EC 3.4.17.11.

OS Pseudomonas sp. RS-16.

XX WO2003045426-A1.

XX 05-JUN-2003.

XX 27-NOV-2002; 2002WO-EP013351.

XX 29-NOV-2001; 2001EP-00128519.

XX 25-JAN-2002; 2002EP-00001778.

XX 13-SEP-2002; 2002EP-00020634.

XX (MERE ) MERCK PATENT GMBH.

XX Hellendoorn K, Baker M, Williams S, Carr FJ;

XX WPI; 2003-513617/48.

XX Claim 3; Page 13; 52pp; English.

CC The invention relates to a novel modified bacterial enzyme  
CC carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2  
CC proteins that are substantially non-immunogenic or less immunogenic than  
CC any non-modified CPG2 having essentially the same biological specificity  
CC when used in vivo, and comprising specific amino acid residues having  
CC alterations compared with the non-modified parochial enzyme. The  
CC alterations cause a reduction or an elimination of one or more of T-cell  
CC epitope sequences, which act in the parental enzyme as MHC class II  
CC binding ligands and stimulate T-cells. The modified CPG2 enzyme and the  
CC CPG2 proteins have immunostimulant activity and may be used in enzyme  
CC therapy. The modified CPG2 enzyme may be used to induce an immune  
CC response in a human host, or as a therapeutic entity such as the gene  
CC directed enzyme prodnug strategy. The peptide is useful for the



CC manufacture of a modified CPG2 enzyme having substantially no or less  
CC immunogenicity than any non-modified parental enzyme when used in vivo,  
CC and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.  
CC This sequence represents a CPG2 enzyme peptide with potential human MHC  
CC class II binding activity of the invention.  
XX  
SQ Sequence 13 AA;

Query Match 49.0%; Score 25; DB 7; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGY 4  
|||  
Db 10 GFGY 13

## RESULT 35

ADC73226  
ID ADC73226 standard; peptide; 14 AA.

XX AC ADC73226;

DT 01-JAN-2004 (first entry)

DE Retro osteogenic growth polypeptide fragment.

XX osteogenic growth polypeptide; OGP analogue; osteoblastic;  
KM fibroblastic cell production; bone formation; osteopenia; fracture;  
KM wound; intraosseous implant; osteoporosis; OGP (1-14); OGP (10-14).

XX Synthetic.

PN WO9732594-A1.

PD 12-SEP-1997.

PF 10-MAR-1997; 97WO-11000087.

PR 10-MAR-1996; 96IL-00117426.

PA (YISS ) YISSUM RES & DEV CO.

PI Bab I, Gazit D, Yu-Chen C, Muhlrud A, Shteyer A, Chorev M;

DR WPI; 1997-470492/43.

PT New osteogenic growth polypeptide analogues - used e.g. for stimulating  
PT the formation of osteoblastic or fibroblastic cells and treating  
PT conditions requiring enhanced bone cell formation.

PS Example; Page 11; 38pp; English.

XX The invention relates to novel pseudopeptidic osteogenic growth  
CC polypeptide (OGP) analogues. The analogues of the invention may be used  
CC for stimulating the formation of osteoblastic or fibroblastic cells,  
CC enhancing bone formation in osteopenia-related pathological conditions,  
CC repairing fractures, healing wounds, grafting of intraosseous implants  
CC and reversing bone loss in osteoporosis and other conditions requiring  
CC enhanced bone cell formation. Furthermore, the analogues may have  
CC activities similar to or superior to that of the parent oligopeptides  
CC OGP (1-14) and OGP (10-14), as well as increased resistance to peptidase  
CC degradation, longer persistence in circulation or increased potency and  
CC bioavailability. The current sequence is that of the retro osteogenic  
CC growth polypeptide fragment of the invention.

SQ Sequence 14 AA;

Query Match 49.0%; Score 25; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGY 4

Db 2 GFGY 5  
|||

RESULT 36  
AAU68422  
ID AAU68422 standard; peptide; 14 AA.

XX AC AAU68422;

DT 16-JAN-2002 (first entry)

DE Human Breast cancer-associated protein isoform, BPI-249 peptide.  
XX Human; Breast cancer-associated protein isoform; breast cancer;  
KM immunogen; cytosstatic; BPI; tryptic digest peptide.

XX Homo sapiens.

PN WO200171357-A2.

PD 27-SEP-2001.

PF 20-MAR-2001; 2001WO-GB001219.

PR 20-MAR-2000; 2000GB-00006695.

PR 24-MAR-2000; 2000GB-00007265.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMAc, O'hare MJ, Page MJ, Parekh RB, Waterfield MD;

DR WPI; 2001-611532/70.

PT Identifying proteins for clinical screening, diagnosis and prognosis of  
PT breast cancer, comprises detecting Breast Cancer-Associated Protein  
PT Isoforms (BPIs) using two-dimensional electrophoresis.

PS Claim 9; Page 52; 197pp; English.

XX The invention relates to diagnosing, determining the stage or severity,  
CC or identifying the risk of a subject developing cancer (especially breast  
CC cancer), or monitoring the effect of therapy on a subject with cancer,  
CC comprising analysing a test sample using two-dimensional electrophoresis  
CC and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The  
CC methods disclosed are used for the diagnosis and prognosis of breast  
CC cancer, for determining the severity of breast cancer, and for  
CC identifying a subject at risk of developing breast cancer, and monitoring  
CC the effect of therapy administered to a subject. Antibodies raised  
CC against the binding domain of a BPI, the binding domain of a BPI, a  
CC nucleic acid encoding a BPI, or a nucleic acid that inhibits the function  
CC of a BPI can be incorporated into a pharmaceutical composition for  
CC treating or preventing breast cancer. The methods use sensitive and  
CC specific biomarkers provide early diagnosis of breast cancer, and the  
CC compositions are more potent, specific, and has a more rapid effect with  
CC fewer side effects than other prior art methods. The present sequence is  
CC a tryptic digest peptide from a BPI of the invention

SQ Sequence 14 AA;

Query Match 49.0%; Score 25; DB 4; Length 14;  
Best Local Similarity 80.0%; Pred. No. 9.8e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYN 6  
|||  
Db 9 FGYN 13

## RESULT 37

AAU25297  
ID AAU25297 standard; peptide; 14 AA.

XX

AC AAU25297;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Schizophrenia-Associated Protein Isoform (SPI) peptide #526.  
XX  
KW Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;  
XX neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.  
XX  
OS Homo sapiens.  
XX  
PN WO200162785-A2.  
XX  
PD 30-AUG-2001.  
XX  
PF 23-FEB-2001; 2001WO-GB000792.  
XX  
PR 24-FEB-2000; 2000GB-00004415.  
XX 28-DEC-2000; 2000US-00750395.  
XX  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX  
PI Herath HMAc, Parekh RB, Rohlf C, Terrett JA, Tyson KL;  
XX  
DR WPI; 2001-570624/64.  
XX  
PT New schizophrenia associated protein isoforms and encoding nucleic acid  
PT molecules, useful for treatment, diagnosis and prognosis of schizophrenia  
PT and screening for potential drugs for treatment and new drug targets.  
XX  
PS Disclosure; Page 39; 148pp; English.  
XX  
CC The sequence represents a schizophrenia-associated protein isoform (SPI).  
CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable  
CC in cerebrospinal fluid, serum or plasma and are useful markers of  
CC schizophrenia. The sequences can be used for treatment and diagnosis of  
CC schizophrenia, screening, prognosis, monitoring the results of therapy,  
CC identifying patients most likely to respond to a particular therapy and  
CC identification of new targets for drug treatment. SPI DNA is useful as a  
CC nucleic acid probe to detect the presence of nucleic acids or SPIs  
XX  
SQ Sequence 14 AA;  
QY  
Db 2 FGYN 6  
9 FGYSN 13

Query Match 49.0%; Score 25; DB 4; Length 14;  
Best Local Similarity 80.0%; Pred. No. 9.8e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 38  
AAU15641  
ID AAU15641 standard; peptide; 14 AA.  
XX  
AC AAU15641;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Schizophrenia-associated isoform peptide #526.  
XX  
KW Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;  
XX neurological disorder; neuropathy.  
XX  
OS Homo sapiens.  
XX  
PN WO200163293-A2.  
XX  
PD 30-AUG-2001.  
XX  
PF 23-FEB-2001; 2001WO-GB000793.  
XX

PR 24-FEB-2000; 2000GB-00004415.  
PR 28-DEC-2000; 2000US-00750395.  
XX  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX  
PI Herath HMAc, Parekh RB, Rohlf C;  
XX  
DR WPI; 2001-502868/55.  
XX  
PT Diagnosing and monitoring Schizophrenia by detecting the presence of  
PT Schizophrenia Associated Features and Schizophrenia Associated Protein  
PT Isoforms in samples of cerebrospinal fluid.  
XX  
PS Claim 6; Page 39; 160pp; English.  
XX  
CC The invention relates to methods and compositions for screening,  
CC diagnosis and prognosis of Schizophrenia. The method involves detecting  
CC the presence of Schizophrenia (SCH) Associated Features (SAs) and SCH  
CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,  
CC immunoassay or hybridisation assay, for diagnosing and monitoring SCH,  
CC studying the effectiveness of treatments and for identifying potential  
CC therapeutic agents. The method is used for (1) screening or diagnosis of  
CC SCH and the relative abundance of at least 1 chosen feature correlates  
CC with the presence or absence of SCH; and (2) monitoring the effect of  
CC therapy administered to a subject with SCH and the relative abundance of  
CC at least 1 chosen feature which correlates with the severity of SCH. The  
CC expression and activity of the SAs, SPIs and related molecules (e.g.  
CC secondary messengers) are studied to diagnose SCH, monitor the progress  
CC of the disorder and the effectiveness of treatment and as targets to  
CC identify and produce potential therapeutic agents for the treatment of  
CC SCH. The paucity of detectable neurologic defects distinguishes  
CC neuropsychiatric disorders such as SCH from neurological disorders, where  
CC manifestations of anatomical and biochemical changes have been identified  
CC in many cases. Consequently the identification and characterisation of  
CC cellular and/or molecular causative defects and neuropathies are  
CC necessary for improved treatment of neuropsychiatric disorders. AAU1514-  
CC AAU15762 represent the amino acid sequences of schizophrenia-associated  
CC isoforms used in the method of the invention  
XX  
SQ Sequence 14 AA;  
QY  
Db 2 FGYN 6  
9 FGYSN 13

Query Match 49.0%; Score 25; DB 4; Length 14;  
Best Local Similarity 80.0%; Pred. No. 9.8e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 39  
ABB52298  
ID ABB52298 standard; peptide; 14 AA.  
XX  
AC ABB52298;  
XX  
DT 08-FEB-2002 (first entry)  
XX  
DE Human API-84 tryptic digest peptide #1.  
XX  
KW Human; neuroprotective; nootropic; gene therapy; vaccine;  
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;  
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;  
KW Expression Reference Protein Isoform; ERPI; proteolysis.  
XX  
OS Homo sapiens.  
XX  
PN WO200175454-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 03-APR-2001; 2001WO-US010908.  
XX



PR 03-APR-2000; 2000US-0194504P.  
XX 28-NOV-2000; 2000US-0253647P.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX (PFI2 ) PFIZER INC.  
PI Durham XL, Friedman DL, Herath HMAc, Kimmel LH, Parekh RB;  
PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;  
XX Townsend RR, White F, Williams SA;  
XX WPI; 2001-639384/73.  
XX  
PT Screening for Alzheimer's disease in a mammal, by making two-dimensional  
PT array of a feature whose relative abundance correlates with disease, and  
PT comparing with abundance of the feature in samples of healthy persons.  
XX  
PS Example; Page 32; 162pp; English.  
XX  
CC The invention relates to methods for the screening, diagnosis and  
CC prognosis of Alzheimer's disease. The methods involve the detection of  
CC Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-  
CC Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or  
CC plasma. The abundance of the AFs and APIs is then normalised to an  
CC Expression Reference Protein Isoform (ERPI) in order to determine whether  
CC a patient is suffering from, or has a predisposition to, Alzheimer's  
CC Disease. The relative abundance of the AFs and APIs correlates with the  
CC severity of Alzheimer's Disease. The present sequence is a peptide  
CC produced from an API by proteolysis  
XX  
SQ Sequence 14 AA;  
XX  
Query Match 49.0%; Score 25; DB 4; Length 14;  
Best Local Similarity 80.0%; Pred. No. 9.8e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 FGYN 6  
Db 9 FGYSN 13  
XX  
RESULT 40  
AAE25488  
ID AAE25488 standard; peptide; 14 AA.  
XX  
AC AAE25488;  
XX  
DT 30-OCT-2002 (first entry)  
XX  
DE CAPI-19 tryptic peptide #2.  
XX  
XX Chronic asthma-associated protein isoform; CAPI; CAF; chronic asthma;  
KM chronic asthma-associated feature; screening; diagnosis; prognosis;  
KM tryptic peptide; therapy.  
XX  
OS Unidentified.  
XX  
PN WO200246768-A2.  
XX  
PD 13-JUN-2002.  
XX  
PF 10-DEC-2001; 2001WO-GB005476.  
XX  
PR 08-DEC-2000; 2000GB-00030051.  
XX  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX  
PI Hall IP, Terrett JA;  
XX  
XX WPI; 2002-537580/57.  
XX  
PT Screening chronic asthma by analyzing a test tissue sample by two  
PT dimensional electrophoresis to generate a two dimensional array of  
PT features and comparing the abundance of the test sample with a sample

PT free from chronic asthma.  
XX  
PS Disclosure; Page 25; 135pp; English.  
XX  
CC The invention relates to a method for screening, diagnosis or prognosis  
CC of chronic asthma using two dimensional electrophoresis to generate a two  
CC dimensional array of features. The invention also provides chronic asthma  
CC -associated protein isoforms (CAPIs) and chronic asthma-associated  
CC features (CAFs) detectable by two dimensional electrophoresis of tissue.  
CC The methods are useful for screening, diagnosis or prognosis of chronic  
CC asthma in a subject, for determining the stage or severity of chronic  
CC asthma, for identifying a subject at risk of developing chronic asthma,  
CC for monitoring the effect of therapy administered to a subject having  
CC chronic asthma and for treating or preventing asthma. They are also used  
CC for the manufacture of a medicament for the treatment or prevention of  
CC chronic asthma. The present sequence is CAPI tryptic peptide  
XX  
SQ Sequence 14 AA;  
XX  
Query Match 49.0%; Score 25; DB 5; Length 14;  
Best Local Similarity 80.0%; Pred. No. 9.8e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 FGYN 6  
Db 9 FGYSN 13  
XX  
RESULT 41  
ABJ15069  
ID ABJ15069 standard; peptide; 14 AA.  
XX  
AC ABJ15069;  
XX  
DT 10-DEC-2002 (first entry)  
XX  
DE Human 125P5C8 epitope #3695.  
XX  
KM Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;  
KM bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.  
XX  
OS Homo sapiens.  
XX  
PN WO200272785-A2.  
XX  
PD 19-SEP-2002.  
XX  
PF 13-MAR-2002; 2002WO-US007855.  
XX  
PR 14-MAR-2001; 2001US-00809638.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Faris M, Challita-Eid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;  
PI Morrison RK, Morrison K, Jakobovits A;  
XX  
DR WPI; 2002-713510/77.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for  
PT treating or preventing cancer that expresses or over expresses 125P5C8.  
XX  
PS Disclosure; Page 216; 274pp; English.  
XX  
CC The present invention relates to compositions comprising a substance that  
CC modulates the status of 125P5C8 or a molecule that is modulated by  
CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The  
CC composition is useful for treating cancer, particularly prostate,  
CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein  
CC and/or a nucleotide sequence encoding the protein is useful for  
CC immunising a mammal against cancer. The present sequence is a 125P5C8  
CC epitope shown in the exemplification of the invention

SQ Sequence 14 AA;

Query Match 49.0%; Score 25; DB 5; Length 14;  
Best Local Similarity 44.4%; Pred. No. 9.8e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFGYKNSKF.9  
| | | | |  
| : : : |  
Db 1 GHNYENTHF 9

## RESULT 42

ABG67720  
ID ABG67720 standard; peptide; 14 AA.

AC ABG67720;

DT 07-OCT-2002 (first entry)

DE Human ADPI tryptic digest peptide #429.

KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;

KW Alzheimer's disease-associated feature; neuroprotective;

KW Alzheimer's disease-associated protein isoform; nootropic;

KW ADPI tryptic digest peptide.

OS Homo sapiens.

PN WO200246767-A2.

PD 13-JUN-2002.

PF 29-NOV-2001; 2001WO-GB005289.

PR 08-DEC-2000; 2000US-0254431P.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMAG, Parekh RB, Rohlf C;

DR WPI; 2002-508575/54.

PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
comprises detecting Alzheimer disease-associated features or Alzheimer  
disease-associated protein isoforms in brain tissue from the subject.

PS Claim 7; Page 63; 427pp; English.

CC The present invention relates to methods and compositions for the  
screening, diagnosis or prognosis of Alzheimer's disease (AD) in a  
subject. The method comprises analysing a sample of brain tissue from a  
subject by 2D electrophoresis to generate a 2D array of Alzheimer's  
disease-associated features (ADFs), whose relative abundance correlates  
with the presence, absence, stage or severity of AD and comparing the  
abundance of each feature with the abundance of that chosen feature in  
brain tissue from persons free from AD. The invention also describes  
Alzheimer's disease-associated protein isoforms (ADPIs) detectable in  
brain tissue. The methods and compositions of the invention are useful  
for the screening, diagnosis or prognosis of AD in a subject, for  
determining the stage or severity of AD in a subject, for identifying a  
subject at risk of developing AD, or for monitoring the effect of therapy  
administered to a subject having AD. Antibodies capable of binding to  
ADPIs are useful for treating or preventing AD, and for determining the  
efficacy of a given treatment regime. An agent that modulates the  
activity of ADPI is useful in the manufacture of a medicament for the  
treatment or prevention of AD in a subject. ABG67292-ABG68038 represent  
human ADPI tryptic digest peptides

SQ Sequence 14 AA;

Query Match 49.0%; Score 25; DB 5; Length 14;  
Best Local Similarity 80.0%; Pred. No. 9.8e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYN 6  
| | | | |  
| : : : |  
Db 9 FGYSN 13

## RESULT 43

ABR91220  
ID ABR91220 standard; peptide; 14 AA.

AC ABR91220;

DT 10-SEP-2003 (first entry)

DE F. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:54.

KW Phlebotomus papatasi; salivary polypeptide; antigenic; immunogenic;  
protozoacide; immunostimulant; vaccine; immune response; Leishmaniasis.

KW Phlebotomus papatasi.

OS Synthetic.

PN WO2002102324-A2.

PD 27-DEC-2002.

PF 18-JUN-2002; 2002WO-US019663.

PR 19-JUN-2001; 2001US-0299391P.

PA (USSH ) US DEPT HEALTH &amp; HUMAN SERVICES.

PI Valenzuela JG, Belkaid Y, Kamhawi S, Sacks D, Ribeiro JMC;

DR WPI; 2003-157000/15.

PT Novel isolated salivary polypeptide of Phlebotomus papatasi, useful for  
producing an immune response in a subject or for preventing Leishmaniasis  
in a subject.

PS Claim 10; Page 80; 279pp; English.

CC The present invention describes an isolated salivary polypeptide (I), of  
Phlebotomus papatasi. Also described: (1) an isolated nucleic acid (II)  
encoding (I); (2) an isolated fragment (III) of (II), where the fragment  
encodes the polypeptide fragment specific for a polypeptide such as  
Phlebotomus papatasi salivary polypeptide (PSP) 12, PSP14, PSP15,  
PSP30, PSP32, PSP36, PSP42 or PSP44; (3) an isolated antigenic or  
immunogenic fragment (IV) of (I); (4) a nucleic acid (V) that hybridises  
under stringent conditions to (II); (5) a vector (VI) comprising (II) or  
(III); and (6) a composition (VII) comprising (I) or its fragment, (IV)  
or (VI), and a pharmaceutically acceptable carrier. (I) has protozoacide  
and immunostimulant activities, and can be used in vaccines. (VII) is  
useful for producing an immune response in a subject or for preventing  
Leishmaniasis in a subject. (II) is also useful for preventing  
Leishmaniasis in a subject. (VII) is useful as a vaccine. ACC79987 to  
ACC79999 and ABR91176 to ABR92046 represent sequences used in the  
exemplification of the present invention

SQ Sequence 14 AA;

Query Match 49.0%; Score 25; DB 6; Length 14;  
Best Local Similarity 37.5%; Pred. No. 9.8e+02;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 FGYN 9

Db 3 YGFANDKY 10

## RESULT 44

ABR59105  
ID ABR59105 standard; peptide; 14 AA.

XX ABR59105;  
AC  
XX 11-JUL-2003 (first entry)  
DT  
XX  
DE Alzheimer's Disease-associated protein isoform, API-84, SEQ ID 240.  
XX  
KW Noctropic; Neuroprotective; Alzheimer's disease; API; human;  
XX Alzheimer's Disease-associated protein isoform.  
OS Homo sapiens.  
XX  
XX WO2003028543-A2.  
PN  
XX  
XX 10-APR-2003.  
PD  
XX  
XX 03-OCT-2002; 2002WO-US031642.  
PF  
XX  
XX 03-OCT-2001; 2001US-0326708P.  
PR  
XX  
XX (PRIZ ) PFIZER PROD INC.  
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX  
XX Durham LK, Friedman D., Herath HMAc, Kimmel LH, Parekh RB;  
PI Potter DM, Rohlf C, Silber BM, Snyder PJ, Soares HD, Stiger TR;  
PI Sunderland PT, Townsend RR, White WF, Williams SA;  
XX  
XX WPI; 2003-371957/35.  
DR  
XX  
XX Screening or diagnosing of Alzheimer's disease (AD) determine the stage  
PT or severity of AD in a subject, comprises analyzing a test sample of body  
PT fluid from the subject by 2-dimensional electrophoresis.  
XX  
XX Claim 2; Page 50; 179pp; English.  
PS  
XX  
XX The present invention relates to methods for screening or diagnosing  
CC Alzheimer's disease (AD) to determine the stage or severity of AD in a  
CC subject, to identify subject at risk of developing AD, or to monitor the  
CC effect of therapy administered. The methods comprise analysing a test  
CC sample of body fluid by 2-dimensional electrophoresis to generate a 2-  
CC dimensional array of AD-associated features (AFs). The method  
CC alternatively comprises quantitatively detecting in a sample of body  
CC fluid from the subject, one or more AD-associated protein isoforms (APIs;  
CC ABR58710-ABR59184)  
XX  
SQ Sequence 14 AA;

Query Match 49.0%; Score 25; DB 6; Length 14;  
Best Local Similarity 80.0%; Pred. No. 9.8e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 FGYN 6  
| | | |  
| | | |  
Db 9 FGYSN 13

RESULT 45  
ADA23853  
ID ADA23853 standard; peptide; 14 AA.  
XX  
XX ADA23853;  
AC  
XX  
XX 20-NOV-2003 (first entry)  
DT  
XX  
XX Alzheimer's disease-associated protein isoform tryptic peptide #462.  
DE  
XX  
XX human; Alzheimer's disease; vascular dementia; Lewy body dementia;  
KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;  
KW Alzheimer's disease-associated protein isoform; ADPI.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2003064411-A1.  
PN

XX  
PD 03-APR-2003.  
XX  
XX 10-DEC-2001; 2001US-00014340.  
PF  
XX  
XX 08-DEC-2000; 2000US-0254431P.  
PR  
XX  
XX (HERA/) HERATH H M A C.  
PA (PARE/) PAREKH R B.  
PA (ROHL/) ROHLFF C.  
XX  
XX Herath HMAc, Parekh RB, Rohlf C;  
PI  
XX  
XX WPI; 2003-540784/51.  
DR  
XX  
XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
PT involves analyzing test sample of brain tissue from subject, and  
PT comparing feature in test sample with that of person(s) free from  
PT Alzheimer's disease.  
XX  
XX Disclosure; SEQ ID NO 462; 115pp; English.  
PS  
XX  
XX The invention relates to a method of screening or diagnosing Alzheimer's  
CC disease in a subject. The method is useful for screening, diagnosis or  
CC prognosis of Alzheimer's disease in a subject for determining the stage  
CC of severity of Alzheimer's disease in a subject, for identifying a  
CC subject at risk of developing Alzheimer's disease, or for monitoring the  
CC effect of therapy administered to a subject having Alzheimer's disease.  
CC The method is also useful in treating vascular dementia, Lewy body  
CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or  
CC depression. The inventive method identifies sensitive and specific  
CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.  
CC It provides therapeutic agents for Alzheimer's disease that works  
CC quickly, potentially, specifically with fewer side effects. The present  
CC sequence represents the amino acid sequence of a Alzheimer's disease-  
CC associated protein isoform tryptic peptide.  
XX  
SQ Sequence 14 AA;

Query Match 49.0%; Score 25; DB 6; Length 14;  
Best Local Similarity 80.0%; Pred. No. 9.8e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 FGYN 6  
| | | |  
| | | |  
Db 9 FGYSN 13

Search completed: August 30, 2004, 10:49:28  
Job time : 17.4088 secs



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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 10.5912 Seconds  
(without alignments)  
327.696 Million cell updates/sec

Title: US-09-720-469A-4  
Perfect score: 60  
Sequence: 1 GYKNSKFRHVI 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3347

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID     | Description         |
|------------|-------|-------------|--------|----|--------|---------------------|
| 1          | 23    | 38.3        | 10     | 6  | Q9TQV4 | Q9TQV4 equus caball |
| 2          | 22    | 36.7        | 12     | 2  | Q53579 | Q53579 rhodobacter  |
| 3          | 22    | 36.7        | 12     | 4  | Q8N6B2 | Q8N6B2 homo sapien  |
| 4          | 22    | 36.7        | 13     | 3  | P87031 | P87031 saccharomyc  |
| 5          | 21    | 35.0        | 12     | 11 | Q8CJ30 | Q8CJ30 mus musculu  |
| 6          | 20    | 33.3        | 14     | 4  | Q9UNM9 | Q9UNM9 homo sapien  |
| 7          | 20    | 33.3        | 14     | 12 | O56127 | O56127 porcine citr |
| 8          | 19    | 31.7        | 10     | 8  | Q8HUB4 | Q8HUB4 anomobryum   |
| 9          | 19    | 31.7        | 12     | 8  | Q8HUB3 | Q8HUB3 bryum donia  |
| 10         | 19    | 31.7        | 14     | 2  | Q50268 | Q50268 phytoplasma  |
| 11         | 18    | 30.0        | 11     | 6  | Q9TUV3 | Q9TUV3 canis famli  |
| 12         | 18    | 30.0        | 11     | 7  | O78121 | O78121 oreochromis  |
| 13         | 18    | 30.0        | 13     | 5  | Q9TWM3 | Q9TWM3 locusta mig  |
| 14         | 18    | 30.0        | 13     | 6  | Q865C9 | Q865C9 sus scrofa   |
| 15         | 18    | 30.0        | 13     | 13 | P82866 | P82866 rana pipien  |
| 16         | 18    | 30.0        | 14     | 10 | P82330 | P82330 pisum sativ  |

|    |    |      |    |    |        |                     |
|----|----|------|----|----|--------|---------------------|
| 17 | 17 | 28.3 | 9  | 5  | Q9TWX7 | Q9twx7 manduca sex  |
| 18 | 17 | 28.3 | 9  | 11 | Q8CG13 | Q8cg13 mus musculu  |
| 19 | 17 | 28.3 | 10 | 2  | Q9X533 | Q9x533 escherichia  |
| 20 | 17 | 28.3 | 10 | 2  | Q9X534 | Q9x534 leclercia a  |
| 21 | 17 | 28.3 | 11 | 10 | Q94IR5 | Q94ir5 pinus radia  |
| 22 | 17 | 28.3 | 12 | 6  | Q9TT31 | Q9tt31 callithrix   |
| 23 | 17 | 28.3 | 12 | 6  | Q9TT29 | Q9tt29 saguinus oe  |
| 24 | 17 | 28.3 | 13 | 2  | Q47601 | Q47601 escherichia  |
| 25 | 17 | 28.3 | 13 | 13 | Q7ZZN6 | Q7zzn6 xenopus lae  |
| 26 | 17 | 28.3 | 14 | 12 | O93202 | O93202 porcine citr |
| 27 | 16 | 26.7 | 8  | 2  | Q44463 | Q44463 rhizobiales  |
| 28 | 16 | 26.7 | 8  | 2  | Q7X4C1 | Q7x4c1 potato wiltc |
| 29 | 16 | 26.7 | 8  | 13 | Q8AWW0 | Q8aww0 coscoroba c  |
| 30 | 16 | 26.7 | 8  | 13 | Q8AWV9 | Q8awv9 anser caeru  |
| 31 | 16 | 26.7 | 8  | 13 | Q8AWV8 | Q8awv8 cygnus colu  |
| 32 | 16 | 26.7 | 8  | 13 | Q8AWV7 | Q8awv7 anas platyr  |
| 33 | 16 | 26.7 | 9  | 8  | Q8MEM3 | Q8mem3 howittia tr  |
| 34 | 16 | 26.7 | 10 | 12 | Q86580 | Q86580 simian para  |
| 35 | 16 | 26.7 | 11 | 3  | Q9UR95 | Q9ur95 pichia angu  |
| 36 | 16 | 26.7 | 11 | 8  | Q8MEL7 | Q8mel7 sida hooker  |
| 37 | 16 | 26.7 | 11 | 8  | Q8MEM2 | Q8mem2 lagunaria p  |
| 38 | 16 | 26.7 | 11 | 8  | Q8MES5 | Q8mes5 abelmoschus  |
| 39 | 16 | 26.7 | 11 | 8  | Q8MEP0 | Q8mep0 hibiscus pe  |
| 40 | 16 | 26.7 | 11 | 8  | Q8MES1 | Q8mes1 alyogyne pi  |
| 41 | 16 | 26.7 | 11 | 8  | Q8MEP3 | Q8mep3 hibiscus no  |
| 42 | 16 | 26.7 | 11 | 8  | Q8MEQ7 | Q8meq7 hibiscus dr  |
| 43 | 16 | 26.7 | 11 | 8  | Q8MEL9 | Q8mel9 pavonia has  |
| 44 | 16 | 26.7 | 11 | 8  | Q8MERO | Q8mer0 hibiscus co  |
| 45 | 16 | 26.7 | 11 | 8  | Q8MES3 | Q8mes3 alyogyne cr  |

ALIGNMENTS

RESULT 1  
Q9TQV4 PRELIMINARY; PRT; 10 AA.  
ID Q9TQV4  
AC Q9TQV4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE POP-variant \* transferin gene, EXON 17 and partial CDS (Fragment).  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Giffard J.M., Brandon R.B., Bell T.K.;  
RT "Further identification of single nucleotide polymorphisms in the  
RT equine transferin gene.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF185778; AAF05491.1; -;  
DR EMBL; AF185770; AAF05483.1; -;  
DR EMBL; AF185771; AAF05484.1; -;  
DR EMBL; AF185772; AAF05485.1; -;  
DR EMBL; AF185773; AAF05486.1; -;  
DR EMBL; AF185774; AAF05487.1; -;  
DR EMBL; AF185775; AAF05488.1; -;  
DR EMBL; AF185776; AAF05489.1; -;  
DR EMBL; AF185777; AAF05490.1; -;  
FT NON TER 1  
SQ SEQUENCE 10 AA; 1188 MW; 6DF67DE9D1AEBDB CRC64;

Query Match 38.3%; Score 23; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FHRV 10  
Db 7 FHRV 10

## RESULT 2

ID Q53579 PRELIMINARY; PRT; 12 AA.  
AC Q53579;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Light-harvesting complex I alpha polypeptide (Fragment).  
GN PUFA.  
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
OC Rhodobacteraceae; Rhodobacter.  
OX NCBI\_TaxID=1061;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92234963; PubMed=1569029;  
RA Richter P., Brand M., Drews G.;  
RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus puFA mutants."  
RT J. Bacteriol. 174:3030-3041(1992).  
RL EMBL; S97551; AAC60405.1; -.  
FT NON TER 12  
SQ SEQUENCE 12 AA; 1627 MW; 0F92F6EA8A70532B CRC64;

Query Match 36.7%; Score 22; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 SKFHRY 10  
ID PRT; 12 AA.

DB 2 SKFYKI 7

## RESULT 3

ID Q8N6B2 PRELIMINARY; PRT; 12 AA.  
AC Q8N6B2;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Capacitative calcium channel protein Trp1 (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Late pregnancy myometrium;  
RX MEDLINE=22181008; PubMed=12193412;  
RA Yang M., Gupta A., Shlykov S.G., Corrigan B., Tsujimoto S.,  
RA Sanborn B.M.;  
RT "Multiple Trp isoforms implicated in capacitative calcium entry are expressed in human pregnant myometrium and myometrial cells."  
RT Biol. Reprod. 67:988-994(2002).  
RL EMBL; AF483645; AAM97860.1; -.  
FT NON TER 1  
SQ SEQUENCE 12 AA; 1511 MW; 4BF47B69BF1B5053 CRC64;

Query Match 36.7%; Score 22; DB 4; Length 12;  
Best Local Similarity 33.3%; Pred. No. 2.5e+03;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKNSKFRH 9  
ID PRT; 13 AA.

DB 1 GYENKTYRK 9

## RESULT 4

ID P87031 PRELIMINARY; PRT; 13 AA.  
AC P87031;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE ORF YGR126W (Fragment).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Van Dyck L., Skala J., de Wergifosse P., Purnelle B., Talla E.,  
RA Nawrocki A., Del Bino S., Goffeau A.;  
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA MIPS;  
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z72912; CAA97139.2; -.  
FT NON TER 1  
SQ SEQUENCE 13 AA; 1594 MW; 2954BA87F3F8C9C8 CRC64;

Query Match 36.7%; Score 22; DB 3; Length 13;  
Best Local Similarity 75.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 FHRV 10  
ID PRT; 12 AA.

DB 8 FHRI 11

## RESULT 5

ID Q8CJ30 PRELIMINARY; PRT; 12 AA.  
AC Q8CJ30;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Myoneurin (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Kidney;  
RX MEDLINE=20334280; PubMed=10873615;  
RA Alliel P.M., Seddigi N., Goudou D., Cifuentes-Diaz C., Romero N.,  
RA Velasco E., Rieger F., Perin J.P.;  
RT "Myoneurin, a novel member of the BTB/POZ-zinc finger family highly expressed in human muscle."  
RT Biochem. Biophys. Res. Commun. 273:385-391(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Kidney;  
RA Bitoun M., Perin J.P., Seddigi N., Goudou D., Camuzat A., Mattei M.G.,  
RA Rieger F., Alliel P.M.;  
RT "The human and mouse myoneurin genes: Genomic organization, splice variants, chromosomal mapping and flanking genes."  
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF530457; AAN28710.1; -.  
FT NON TER 1  
FT NON TER 12  
SQ SEQUENCE 12 AA; 1448 MW; 5A48D26D86A331E3 CRC64;

Query Match 35.0%; Score 21; DB 11; Length 12;  
Best Local Similarity 57.1%; Pred. No. 3.9e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKFRH 9  
ID PRT; 7

DB 1 KNLKKGK 7

## RESULT 6

Q9UNM9

```
ID Q9UNM9 PRELIMINARY; PRT; 14 AA.
AC Q9UNM9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE RING3 protein (Fragment).
GN RING3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Keddache M, Zhang F, Greenberg D.A.;
RT "A Dinucleotide Repeat Between Exons 2 and 3 of the Human RING3
RT Gene."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF107699; AAD24963.1; -.
DR InterPro; IPR001487; Bromodomain.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1677 MW; 5CDF036680AE22D3 CRC64;

Query Match
Best Local Similarity 33.3%; Score 20; DB 4; Length 14;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 FHRVI 11
Db 2 YHKII 6

RESULT 7
ID Q56127 PRELIMINARY; PRT; 14 AA.
AC Q56127;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ORF11.
OS Porcine circovirus.
OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
OX NCBI_TaxID=46221;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=pms PCV;
RX MEDLINE=98241772; PubMed=9573301;
RA Hamel A.L., Lin L.L., Nayar G.P.;
RT "Nucleotide sequence of porcine circovirus associated with postweaning
RT multisystemic wasting syndrome in pigs."
RL J. Virol. 72:5262-5267(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=pms PCV;
RX Hamel A.L., Lin L.L., Nayar G.P.S.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF027217; AAC59472.1; -.
SQ SEQUENCE 14 AA; 1761 MW; 00F50DC89EBAF20B CRC64;

Query Match
Best Local Similarity 33.3%; Score 20; DB 12; Length 14;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSKPHRVI 11
Db 2 KNKNHYEVI 10

RESULT 8
ID Q8HUB4 PRELIMINARY; PRT; 10 AA.
AC Q8HUB4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
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DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Ribosomal protein L16 (Fragment).
GN RPL16.
OS Anomobryum julaceum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Bryales; Bryaceae; Anomobryum.
OX NCBI_TaxID=67232;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Aj607;
RA Pedersen N., Cox C., Hedenas L.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF546765; AAN62980.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1326 MW; 6314C32409C321B4 CRC64;

Query Match
Best Local Similarity 31.7%; Score 19; DB 8; Length 10;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKPHR 9
Db 2 KRTKFRK 8

RESULT 9
ID Q8HU93 PRELIMINARY; PRT; 12 AA.
AC Q8HU93;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Ribosomal protein L16 (Fragment).
GN RPL16.
OS Bryum donianum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Bryales; Bryaceae; Bryum.
OX NCBI_TaxID=66993;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BD628;
RA Pedersen N., Cox C., Hedenas L.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF546786; AAN63001.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1539 MW; 5F27C314C32409C3 CRC64;

Query Match
Best Local Similarity 31.7%; Score 19; DB 8; Length 12;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKPHR 9
Db 2 KRTKFRK 8

RESULT 10
ID Q50268 PRELIMINARY; PRT; 14 AA.
AC Q50268;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Rpl16 protein (Fragment).
```

GN RPL16.  
OS Phycoplasma sp.  
OC Bacteria; Firmicutes; Mollicutes; Achleoplasmatales;  
OC Achleoplasmatales; Phycoplasma.  
OX NCBI\_TaxID=2155;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lim P.-O., Sears B.B.;  
RT "DNA sequence of the ribosomal protein genes rpl2 and rpl9 from a  
RL plant-pathogenic mycoplasma-like organism.";  
RN FEWS Microbiol. Lett. 84:71-74(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92210505; PubMed=1556079;  
RA Lim P.-O., Sears B.B.;  
RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like  
RL organism and Achleoplasmatales deduced from two ribosomal protein  
RT gene sequences.";  
RL J. Bacteriol. 174:2606-2611(1992).  
DR EMBL; M74770; AAA25331.1; -.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1870 MW; 87C3153B73386A21 CRC64;

Query Match 31.7%; Score 19; DB 2; Length 14;  
Best Local Similarity 42.3%; Pred. No. 1.1e+04;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKPHR 9  
| : | : |  
Db 5 KRTKYRR 11

## RESULT 11

ID Q9TU3 PRELIMINARY; PRT; 10 AA.  
AC Q9TU3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE BRCA1 (Fragment).  
GN BRCA1.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20154965; PubMed=10690375;  
RA Gray I.S., Yuzbasiyan-Gurkan V.;  
RT "A single nucleotide (T->G) polymorphism within intron 23 of the  
RL canine BRCA1 gene.";  
RL Anim. Genet. 31:76-77(2000).  
DR EMBL; AF159258; AAD56289.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1164 MW; 2AB89C65BAAB01B3 CRC64;

Query Match 30.0%; Score 18; DB 6; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSKPHR 8  
| : | : |  
Db 5 EDSGFH 10

## RESULT 12

ID 078121 PRELIMINARY; PRT; 11 AA.  
AC 078121;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE MHC class II B locus 12 (Fragment).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98315113; PubMed=9649539;  
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
RA Figueroa F., Sultmann H., Klein J.;  
RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
RL class II B loci.";  
RL Genetics 149:1527-1537(1998).  
DR EMBL; AF050027; AAC41366.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1362 MW; 03C12D8EB7341B54 CRC64;

Query Match 30.0%; Score 18; DB 7; Length 11;  
Best Local Similarity 33.3%; Pred. No. 1.3e+04;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYKSKPHR 9  
| : | : |  
Db 1 GFMYRLSR 9

## RESULT 13

ID Q9TWM3 PRELIMINARY; PRT; 13 AA.  
AC Q9TWM3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE LOCUSTAMYOINIBIN, LOW-MH-MYOINIBITING neuropeptide.  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95063174; PubMed=7972937;  
RA Schoofs L., Veeleart D., Holman G.M., Hayes T.K., De Loof A.;  
RT "Partial identification, synthesis and immunolocalization of  
RT locustamyoininibin, the third myoinhibiting neuropeptide isolated from  
RL locusta migratoria.";  
RL Regul. Pept. 52:139-156(1994).  
SQ SEQUENCE 13 AA; 1464 MW; D84ABBE624DC5A6 CRC64;

Query Match 30.0%; Score 18; DB 5; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.5e+04;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSKPHRV 10  
| : | : |  
Db 5 KQSAFNAV 12

## RESULT 14

ID Q865C9 PRELIMINARY; PRT; 13 AA.  
AC Q865C9;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Glutamine synthetase (Fragment).  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
OX NCBI\_TaxID=9823;



RN [1]  
RP SEQUENCE FROM N.A.  
RA Kim J.G., Vallet J.L., Christenson R.K.;  
RT "Characterization of porcine glutamine synthetase."  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY216477; AA064254.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 13 AA; 1555 MW; 87987A0B71AB6B1A CRC64;

Query Match 30.0%; Score 18; DB 6; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKN 4  
Db 11 YKN 13

RESULT 15  
P82866 PRELIMINARY; PRT; 13 AA.  
AC P82866;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE RNA-binding protein (Fragment).  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OX NCBI\_TaxID=8404;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Embryonic epithelium;  
RA Banerjee H.N., Blackmon R.H., Moses A., Harmon G.L., Peterson B.L.,  
RA Khan A.;  
RT "Isolation, identification and characterization of a novel 5'UTR  
RT binding protein for VCAM-1."  
RL Submitted (NOV-2000) to Swiss-Prot.  
CC -1- FUNCTION: BINDS TO THE VCAM-1 5'UTR REGION.  
CC -1- SIMILARITY: TO THE FETUIN FAMILY.  
CC PIR; A59387; A59387.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR InterPro; IPR001363; Fetuin.  
DR PROSITE; PS01254; FETUIN\_1; PARTIAL.  
DR PROSITE; PS01255; FETUIN\_2; PARTIAL.  
KW RNA-binding.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1370 MW; C683612A61757DC2 CRC64;

Query Match 30.0%; Score 18; DB 13; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYK 3  
Db 8 GYK 10

RESULT 16  
P82330 PRELIMINARY; PRT; 14 AA.  
AC P82330;  
DT 01-JUN-2000 (TREMBLrel. 14, Created)  
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Unknown protein from 2D-page of thylakoid PERIPHERY (SPOT112)  
DE (Fragment).  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]

RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;  
RX MEDLINE=20181728; PubMed=10715320;  
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,  
RA Adamska I., van Wijk K.J.;  
RT "Proteomics of the chloroplast: systematic identification and  
RT targeting analysis of luminal and peripheral thylakoid proteins."  
RL Plant Cell 12:319-341(2000).  
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE PERIPHERY.  
CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 6, ITS MW IS: 22.9 KDA.  
DR GO; GO:0009507; C:chloroplast; IEA.  
DR GO; GO:0009579; C:thylakoid; IEA.  
KW Chloroplast; Thylakoid.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1405 MW; 8051E964D580014A CRC64;

Query Match 30.0%; Score 18; DB 10; Length 14;  
Best Local Similarity 44.4%; Pred. No. 1.6e+04;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSKPHRYI 11  
Db 3 KGSSDNRYL 11

RESULT 17  
Q9TXX7 PRELIMINARY; PRT; 9 AA.  
AC Q9TXX7;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Juvenile hormone binding protein, JHBP=4.9 kDa GLU-C peptide  
DE (Fragment).  
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;  
OC Sphingidae; Sphinginae; Manduca.  
OX NCBI\_TaxID=7130;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92134256; PubMed=1734862;  
RA Tsuchihara K., Prestwich G.D.;  
RT "Binding site mapping of a photoaffinity-labeled juvenile hormone  
RT binding protein."  
RL Biochem. Biophys. Res. Commun. 182:466-473(1992).  
FT NON\_TER 1 1  
SQ SEQUENCE 9 AA; 1023 MW; E063C40045A2D401 CRC64;

Query Match 28.3%; Score 17; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 HRV 10  
Db 2 HRV 4

RESULT 18  
Q8CG13 PRELIMINARY; PRT; 9 AA.  
AC Q8CG13;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Glutamate receptor ionotropic N-methyl D-aspartate-like 1A  
DE (Fragment).  
GN GRIN1A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7BL/6J;  
 RA Wyder K.S., Mohan Raj B.K., Sciorra L.J., Roginski R.S.;  
 RT "The mouse orthologue of the human ionotropic glutamate receptor-like  
 gene (GRIN1A) maps to mouse chromosome 9.";  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF462417; AAO15648.1; -  
 DR EMBL: AF462416; AAO15648.1; JOINED.  
 DR MGI:107282; Grin1a.  
 DR GO: GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1091 MW; 6A91233EB059C33B CRC64;

Query Match 28.3%; Score 17; DB 11; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSKF 7  
 |||  
 Db 1 NEKF 4

RESULT 19  
 Q9X533 PRELIMINARY; PRT; 10 AA.  
 ID Q9X533  
 AC Q9X533;  
 DT 01-NOV-1999 (TReMBLrel. 12, Created)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Periplasmic mercuric ion binding protein (Fragment).  
 GN MERP.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=209A;  
 RX MEDLINE=97208220; PubMed=9055422;  
 RA Liebert C.A., Wireman J., Smith T., Summers A.O.;  
 RT "Phylogeny of mercury resistance (mer) operons of gram-negative  
 bacteria isolated from the fecal flora of primates.";  
 RL Appl. Environ. Microbiol. 63:1066-1076(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=209A;  
 RX MEDLINE=98027386; PubMed=9361435;  
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;  
 RT "Association of mercury resistance with antibiotic resistance in the  
 gram-negative fecal bacteria of primates.";  
 RL Appl. Environ. Microbiol. 63:4494-4503(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=209A;  
 RX MEDLINE=20568355; PubMed=11116334;  
 RA Liebert C.A., Watson A.L., Summers A.O.;  
 RT "The quality of merC, a module of the mer mosaic.";  
 RL J. Mol. Evol. 51:607-622(2000).  
 DR EMBL: AF120964; AAD23783.1; -  
 FT NON\_TER 1 1  
 FT NON\_TER 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;  
 SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;

Query Match 28.3%; Score 17; DB 2; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 1.8e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKNS 5  
 |||

Db 3 GYPSS 7  
 RESULT 20  
 Q9X534 PRELIMINARY; PRT; 10 AA.  
 ID Q9X534  
 AC Q9X534;  
 DT 01-NOV-1999 (TReMBLrel. 12, Created)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Periplasmic mercuric ion binding protein (Fragment).  
 GN MERP.  
 OS Leclercia adecarboxylata.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Leclercia.  
 OX NCBI\_TaxID=83655;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=742H;  
 RX MEDLINE=97208220; PubMed=9055422;  
 RA Liebert C.A., Wireman J., Smith T., Summers A.O.;  
 RT "Phylogeny of mercury resistance (mer) operons of gram-negative  
 bacteria isolated from the fecal flora of primates.";  
 RL Appl. Environ. Microbiol. 63:1066-1076(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=742H;  
 RX MEDLINE=98027386; PubMed=9361435;  
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;  
 RT "Association of mercury resistance with antibiotic resistance in the  
 gram-negative fecal bacteria of primates.";  
 RL Appl. Environ. Microbiol. 63:4494-4503(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=742H;  
 RX MEDLINE=20568355; PubMed=11116334;  
 RA Liebert C.A., Watson A.L., Summers A.O.;  
 RT "The quality of merC, a module of the mer mosaic.";  
 RL J. Mol. Evol. 51:607-622(2000).  
 DR EMBL: AF120965; AAD23785.1; -  
 FT NON\_TER 1 1  
 FT NON\_TER 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;  
 SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;

Query Match 28.3%; Score 17; DB 2; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 1.8e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKNS 5  
 |||  
 Db 3 GYPSS 7

RESULT 21  
 Q94IR5 PRELIMINARY; PRT; 11 AA.  
 ID Q94IR5  
 AC Q94IR5;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Nonspecific lipid transfer protein (Fragment).  
 OS Pinus radiata (Monterey pine).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
 OX NCBI\_TaxID=3347;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PRLTP9-1158055;  
 RA Jones D.F.;  
 RT "Genetic mapping of the lipid transfer protein gene family in Pinus  
 radiata and Pinus taeda.";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY029028; AAK40266.1; -  
 FT NON\_TER 11 11

SQ SEQUENCE 11 AA; 1361 MW; 471B518D473AE727 CRC64;

Query Match 28.3%; Score 17; DB 10; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.9e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NSKF 7  
|:|:  
8 NSQF 11

RESULT 22

Q9TT31 PRELIMINARY; PRT; 12 AA.

AC Q9TT31; 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Beta-globin (Fragment).  
OS Callithrix jacchus (Common marmoset).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.  
OX NCBI\_TaxID=9483;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=20188801; PubMed=10723742;  
RA Francino M.P., Ochman H.;  
RT "Strand Symmetry around the beta-Globin Origin of Replication in  
RT Primates";  
RL Mol. Biol. Evol. 17:416-422(2000).  
DR EMBL; AF205413; AAF23764.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 12 AA; 1251 MW; 07BC8AFAE8D72DD4 CRC64;

Query Match 28.3%; Score 17; DB 6; Length 12;  
Best Local Similarity 33.3%; Pred. No. 2.1e+04;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYKNSKFHR 9  
|:|:  
Db 2 GVANALAHK 10

RESULT 23

Q9TT29 PRELIMINARY; PRT; 12 AA.

AC Q9TT29; 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Beta-globin (Fragment).  
OS Saguinus oedipus (Cotton-top tamarin).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.  
OX NCBI\_TaxID=9490;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=20188801; PubMed=10723742;  
RA Francino M.P., Ochman H.;  
RT "Strand Symmetry around the beta-Globin Origin of Replication in  
RT Primates";  
RL Mol. Biol. Evol. 17:416-422(2000).  
DR EMBL; AF205415; AAF23766.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 12 AA; 1251 MW; 07BC8AFAE8D72DD4 CRC64;

Query Match 28.3%; Score 17; DB 6; Length 12;  
Best Local Similarity 33.3%; Pred. No. 2.1e+04;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYKNSKFHR 9

Db 2 GVANALAHK 10

RESULT 24

Q47601 PRELIMINARY; PRT; 13 AA.

AC Q47601; 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE C (Fragment).  
GN C.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91139577; PubMed=1995588;  
RA Tao T., Bourne J.C., Blumenthal R.M.;  
RT "A family of regulatory genes associated with type II restriction-  
RT modification systems";  
RL J. Bacteriol. 173:1367-1375(1991).  
DR EMBL; M63620; AAA24557.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 13 AA; 1485 MW; DABC813667902866 CRC64;

Query Match 28.3%; Score 17; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.3e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKNSK 6  
|:|:  
Db 7 GLKNEQ 12

RESULT 25

Q7ZZN6 PRELIMINARY; PRT; 13 AA.

AC Q7ZZN6; 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Zinc finger protein (Fragment).  
GN ZIC3.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cerebellum;  
RA Weber J.R., Sokol S.Y.;  
RT "Identification of a phylogenetically conserved activin-responsive  
RT enhancer in the Zic3 gene";  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF506278; AAP20809.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 13 AA; 1537 MW; 5DDA56257F6DF2C3 CRC64;

Query Match 28.3%; Score 17; DB 13; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.3e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKFH 8  
|:|:  
Db 3 KHKVH 8

RESULT 26

O93202  
ID O93202 PRELIMINARY; PRT; 14 AA.  
AC O93202; O9YU34;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE ORF11.  
OS Porcine circovirus,  
OS Porcine circovirus type 2-D,  
OS Porcine circovirus type 2-C,  
OS Porcine circovirus type 2-E,  
OS Porcine circovirus type 2-B,  
OS Bovine circovirus, and  
OS Porcine circovirus type 2.  
OC Viruses; ssDNA viruses; Circoviridae; Circovirus.  
OX NCBI\_TaxID=46221, 86385, 85543, 85544, 85709, 85542, 85708;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=porcine circovirus; STRAIN=PORCINE CIRCOVIRUS TYPE II;  
RX MEDLINE=98418498; PubMed=9747726;  
RA Meenan B.M., McNeilly F.M., Todd D., Kennedy S., Jewhurst V.,  
RA Ellis J.A., Hassard L.E., Clark E.G., Haines D.M., Allan G.M.;  
RT "Characterization of novel circovirus DNAs associated with wasting  
syndromes in pigs.";  
RL J. Gen. Virol. 79:2171-2199 (1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=porcine circovirus; STRAIN=PORCINE CIRCOVIRUS TYPE II;  
RA Meenan B.M.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=porcine circovirus type 2-D;  
RA Hamel A.L., Nayar G.P.S.;  
RT "Genetic characterization of four novel type-2 Porcine circoviruses.";  
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC SPECIES=porcine circovirus type 2-C, and porcine circovirus type 2-E;  
RA Hamel A.L., Nayar G.P.S.;  
RT "Nucleotide sequence of four different isolates of circovirus detected  
in pigs with various clinical syndromes.";  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC SPECIES=porcine circovirus type 2-B;  
RA Hamel A.L., Nayar G.P.S.;  
RT "Nucleotide sequence of four different isolates of porcine circovirus  
detected in pigs with various clinical syndromes.";  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC SPECIES=bovine circovirus;  
RA Hamel A.L., Nayar G.P.S.;  
RT "Nucleotide sequence of a circovirus detected in cattle with various  
clinical syndromes.";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RC SPECIES=porcine circovirus type 2; STRAIN=24657 NL;  
RA Wellenberg G.J., Pesch S., Berndsen F.W., Steverink P.J.G.M.,  
RA Hunneman W., Van der Vorst T.J.K., Peperkamp N.H.M.T., Ohlinger V.F.,  
RA Schippers R., Van Oirschot J.T., de Jong M.F.;  
RT "Isolation and characterization of porcine circovirus type 2 from pigs  
showing signs of post-weaning multisystemic wasting syndrome in The  
Netherlands.";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF055394; AAC35336.1; -;  
DR EMBL; AF055391; AAC35305.1; -;  
DR EMBL; AF055392; AAC35316.1; -;  
DR EMBL; AF055393; AAC35326.1; -;  
DR EMBL; AF117753; AAD12313.1; -;  
DR EMBL; AF109398; AAD03069.1; -;

DR EMBL; AF109399; AAD03080.1; -;  
DR EMBL; AF112862; AAD03090.1; -;  
DR EMBL; AF109397; AAD11937.1; -;  
DR EMBL; AF201897; AAG41230.1; -;  
SQ SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 28.3%; Score 17; DB 12; Length 14;  
Best Local Similarity 60.0%; Pred. No. 2.5e+04;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 NSKFH 8  
| | | |  
Db 2 NNKNH 6

## RESULT 27

O44463  
ID O44463 PRELIMINARY; PRT; 8 AA.  
AC O44463;

DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Agrobacterium tumefaciens Ti plasmid virD3 and virD4 genes  
(Fragment).  
OS Rhizobiales (rhizobacteria).  
OG plasmid Ti.  
OC Bacteria; Proteobacteria; Alphaproteobacteria.  
OX NCBI\_TaxID=356;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88015611; PubMed=3658701;  
RA Portner S.G., Yanofsky M.F., Nester E.W.;  
RT "molecular characterization of the virD operon from Agrobacterium  
tumefaciens.";  
RL Nucleic Acids Res. 15:7503-7517 (1987).  
DR EMBL; X06045; CAA29439.1; -;  
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
KW Plasmid.  
FT NON TER  
SQ SEQUENCE 8 AA; 887 MW; F8F2C325B33861A6 CRC64;

Query Match 26.7%; Score 16; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1e+06;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 SKFH 8  
| | | |  
Db 5 SKVH 8

## RESULT 28

O7X4C1  
ID O7X4C1 PRELIMINARY; PRT; 8 AA.  
AC O7X4C1;

DT 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Ribosomal protein S19 (Fragment).  
GN RPS19.  
OS Potato witches'-broom phytoplasma.  
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
OC Acholeplasmataceae; Phytoplasma.  
OX NCBI\_TaxID=37701;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FMB;  
RA Lee I.-M., Martini M., Marcone C., Zhu S.;

RT "Classification of phytoplasma strains in the elm yellows group  
(16S-rv) and proposition of 'Candidatus Phytoplasma ulmi' for the  
RT phytoplasma associated with elm yellows and 'Candidatus Phytoplasma  
RT chinense' for the phytoplasma associated with cherry lethal yellowing  
in China.";  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY197682; AAP42406.1; -.  
KM Ribosomal protein.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 945 MW; 783326D443333AA8 CRC64;

Query Match  
Best Local Similarity 26.7%; Score 16; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1e+06;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSK 6  
DB 4 KNQK 7

RESULT 29

Q8AWW0 PRELIMINARY; PRT; 8 AA.  
AC Q8AWW0;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE LDH-B (Fragment).  
GN LDH-B.  
OS Coscoroba coscoroba (Coscoroba swan).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Coscoroba.  
OX NCBI\_TaxID=8863;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Cotter J.-P., StJohn J., Quinn T.W.;  
RT "Isolation of a Precisely Delineated, Recently Transposed Chicken  
RT Repeat 1 (CRI) Retrotransposon Within an Intron of the Coscoroba  
RT coscoroba.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY123324; AAM96898.1; -.  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match  
Best Local Similarity 26.7%; Score 16; DB 13; Length 8;  
Best Local Similarity 25.0%; Pred. No. 1e+06;  
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 HRVI 11  
DB 2 HKIV 5

RESULT 30

Q8AWV9 PRELIMINARY; PRT; 8 AA.  
AC Q8AWV9;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE LDH-B (Fragment).  
GN LDH-B.  
OS Anser caerulescens caerulescens (snow goose).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.  
OX NCBI\_TaxID=70340;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Cotter J.-P., StJohn J., Quinn T.W.;  
RT "Isolation of a Precisely Delineated, Recently Transposed Chicken  
RT Repeat 1 (CRI) Retrotransposon Within an Intron of the Coscoroba  
RT coscoroba.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY123325; AAM96899.1; -.  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match  
Best Local Similarity 26.7%; Score 16; DB 13; Length 8;  
Best Local Similarity 25.0%; Pred. No. 1e+06;  
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 HRVI 11  
DB 2 HKIV 5

RESULT 31

Q8AWV8 PRELIMINARY; PRT; 8 AA.  
AC Q8AWV8;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE LDH-B (Fragment).  
GN LDH-B.  
OS Cygnus columbianus (tundra swan).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Cygnus.  
OX NCBI\_TaxID=110926;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Cotter J.-P., StJohn J., Quinn T.W.;  
RT "Isolation of a Precisely Delineated, Recently Transposed Chicken  
RT Repeat 1 (CRI) Retrotransposon Within an Intron of the Coscoroba  
RT coscoroba.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY123326; AAM96900.1; -.  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match  
Best Local Similarity 26.7%; Score 16; DB 13; Length 8;  
Best Local Similarity 25.0%; Pred. No. 1e+06;  
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 HRVI 11  
DB 2 HKIV 5

RESULT 32

Q8AWV7 PRELIMINARY; PRT; 8 AA.  
AC Q8AWV7;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE LDH-B (Fragment).  
GN LDH-B.  
OS Anas platyrhynchos (Domestic duck).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.  
OX NCBI\_TaxID=8839;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Cotter J.-P., StJohn J., Quinn T.W.;  
RT "Isolation of a Precisely Delineated, Recently Transposed Chicken  
RT Repeat 1 (CRI) Retrotransposon Within an Intron of the Coscoroba  
RT coscoroba.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY123327; AAM96901.1; -.  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match  
Best Local Similarity 26.7%; Score 16; DB 13; Length 8;  
Best Local Similarity 25.0%; Pred. No. 1e+06;  
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 HRVI 11

Db 2 HKIV 5

RESULT 33

Q8MEM3 PRELIMINARY; PRT; 9 AA.  
AC Q8MEM3;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Howittia trilocularis.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Howittia.  
OX NCBI\_TaxID=183272;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384615; AAM50387.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1256 MW; 6351D32409D411B4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 9;  
Best Local Similarity 28.6%; Pred. No. 1e+06; 2; Indels 0; Gaps 0;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKFR 9  
Db 1 KRTRFRK 7

RESULT 34

Q86580 PRELIMINARY; PRT; 10 AA.  
AC Q86580;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE Large protein (Fragment).  
OS Simian parainfluenza virus 5.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.  
OX NCBI\_TaxID=11207;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=93224905; PubMed=8385701;  
RA Higuchi Y., Miyahara Y., Kawano M., Tsurudome M., Matsumura H.,  
RA Kusagawa S., Komada H., Nishio M., Ito Y.;  
RT "Sequence analysis of the large (L) protein of simian virus 5.";  
RL J. Gen. Virol. 74:789-799(1993).  
DR EMBL; S57860; AAB26118.1; -  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1144 MW; 0C25A0D9C86776D4 CRC64;

Query Match 26.7%; Score 16; DB 12; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.7e+04;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYKN 4  
Db 6 GFQN 9

RESULT 35

Q9UR95 PRELIMINARY; PRT; 11 AA.  
AC Q9UR95;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
DE Heat shock protein 60 homolog (Fragment).  
OS Pichia angusta (Yeast) (Hansenula polymorpha).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Pichia.  
OX NCBI\_TaxID=4905;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93223840; PubMed=8096822;  
RA Evers M.E., Hulse B., Titorenko V.I., Kunau W.H., Hartl F.U.,  
RA Harder W., Veenhuis M.;  
RT "Affinity purification of molecular chaperones of the yeast Hansenula  
RT polymorpha using immobilized denatured alcohol oxidase.";  
RL FEBS Lett. 321:32-36(1993).  
SQ SEQUENCE 11 AA; 1230 MW; 71872C1779C3372B CRC64;

Query Match 26.7%; Score 16; DB 3; Length 11;  
Best Local Similarity 50.0%; Pred. No. 3e+04; 2; Indels 0; Gaps 0;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKSKF 7  
Db 2 HKELKF 7

RESULT 36

Q8MEL7 PRELIMINARY; PRT; 11 AA.  
AC Q8MEL7;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Sida hookeriana.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Sida.  
OX NCBI\_TaxID=108446;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384624; AAM50396.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;  
Best Local Similarity 28.6%; Pred. No. 3e+04;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKFR 9  
Db 1 KRTRFRK 7

RESULT 37

Q8MEM2 PRELIMINARY; PRT; 11 AA.  
AC Q8MEM2;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Lagunaria patersonia.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Lagunaria.  
OX NCBI\_TaxID=183274;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384616; AAM50388.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;  
Best Local Similarity 28.6%; Pred. No. 3e+04;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 KNSKFHR 9  
|::|:  
Db 1 KRTRFRK 7

## RESULT 38

Q8MESS  
ID Q8MESS PRELIMINARY; PRT; 11 AA.  
AC Q8MESS;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Abelmoschus manihot.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Abelmoschus.  
OX NCBI\_TaxID=183220;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384561; AAM50399.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;  
Best Local Similarity 28.6%; Pred. No. 3e+04;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 KNSKFHR 9  
|::|:  
Db 1 KRTRFRK 7

## RESULT 39

Q8MEP0  
ID Q8MEP0 PRELIMINARY; PRT; 11 AA.  
AC Q8MEP0;

DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Hibiscus peralbus.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.  
OX NCBI\_TaxID=183256;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384598; AAM50370.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;  
Best Local Similarity 28.6%; Pred. No. 3e+04;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 KNSKFHR 9  
|::|:  
Db 1 KRTRFRK 7

## RESULT 40

Q8MES1  
ID Q8MES1 PRELIMINARY; PRT; 11 AA.  
AC Q8MES1;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Alyogyne pinoniana.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Alyogyne.  
OX NCBI\_TaxID=183226;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384566; AAM50404.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;  
Best Local Similarity 28.6%; Pred. No. 3e+04;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 KNSKFHR 9  
|::|:  
Db 1 KRTRFRK 7

## RESULT 41

Q8MEP3  
ID Q8MEP3 PRELIMINARY; PRT; 11 AA.  
AC Q8MEP3;



AC Q8MEP3; 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Hibiscus normanii.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.  
OX NCBI\_TaxID=183253;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384595; AAMS0367.1; -;  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;  
Best Local Similarity 28.6%; Pred. No. 3e+04;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKPR 9  
| : : | :  
Db 1 KRTRPRK 7

## RESULT 42

Q8MEQ7 PRELIMINARY; PRT; 11 AA.  
ID Q8MEQ7;  
AC Q8MEQ7;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Hibiscus drummondii.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.  
OX NCBI\_TaxID=183239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384581; AAMS0353.1; -;  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;  
Best Local Similarity 28.6%; Pred. No. 3e+04;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKPR 9  
| : : | :  
Db 1 KRTRPRK 7

## RESULT 43

Q8MEL9

ID Q8MEL9 PRELIMINARY; PRT; 11 AA.  
AC Q8MEL9; 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Pavonia hastata.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Pavonia.  
OX NCBI\_TaxID=183278;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384622; AAMS0394.1; -;  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;  
Best Local Similarity 28.6%; Pred. No. 3e+04;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKPR 9  
| : : | :  
Db 1 KRTRPRK 7

## RESULT 44

Q8MER0 PRELIMINARY; PRT; 11 AA.  
ID Q8MER0;  
AC Q8MER0;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Hibiscus coatesii.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.  
OX NCBI\_TaxID=183236;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384578; AAMS0416.1; -;  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 26.7%; Score 16; DB 8; Length 11;  
Best Local Similarity 28.6%; Pred. No. 3e+04;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKPR 9  
| : : | :  
Db 1 KRTRPRK 7

## RESULT 45

Q8MEL9



Q8MES3  
ID Q8MES3 PRELIMINARY; PRT; 11 AA.  
AC Q8MES3;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Ribosomal protein 16 (Fragment).  
GN RPL16.  
OS Alyogyne cravenii.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Alyogyne.  
OX NCBI\_TaxID=183223;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;  
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using  
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";  
RL Syst. Bot. 27:333-350(2002).  
DR EMBL; AF384563; AAM50401.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;  
Query Match 26.7%; Score 16; DB 8; Length 11;  
Best Local Similarity 28.6%; Pred. No. 3e+04;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 3 KNSKFRH 9  
|::|:  
Db 1 KRTRPRK 7

Search completed: August 30, 2004, 10:55:18  
Job time : 12.5912 secs



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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:09 ; Search time 1.89527 Seconds  
(without alignments)  
302.211 Million cell updates/sec

Title: US-09-720-469A-4  
Perfect score: 60  
Sequence: 1 GYKNSKPHRV 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 585

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 21    | 35.0        | 10     | 1  | TKNB_RANCA  |
| 2          | 20    | 33.3        | 12     | 1  | FAR7_PENMO  |
| 3          | 20    | 33.3        | 13     | 1  | LMAL_LOCOMI |
| 4          | 19    | 31.7        | 8      | 1  | COXG_RAT    |
| 5          | 19    | 31.7        | 10     | 1  | FAR7_MACRS  |
| 6          | 19    | 31.7        | 14     | 1  | MY14_EISFO  |
| 7          | 18    | 30.0        | 8      | 1  | LCK6_LEUMA  |
| 8          | 18    | 30.0        | 11     | 1  | ASL1_BACSE  |
| 9          | 18    | 30.0        | 11     | 1  | CXL1_CONMR  |
| 10         | 18    | 30.0        | 13     | 1  | CXL4_CONMR  |
| 11         | 17    | 28.3        | 9      | 1  | FARP_CALSI  |
| 12         | 17    | 28.3        | 10     | 1  | COXM_RAT    |
| 13         | 17    | 28.3        | 11     | 1  | EFG_CLOPA   |
| 14         | 17    | 28.3        | 11     | 1  | NXSN_PSETE  |
| 15         | 17    | 28.3        | 14     | 1  | MY14_PHEVI  |
| 16         | 16    | 26.7        | 8      | 1  | LCK4_LEUMA  |
| 17         | 16    | 26.7        | 10     | 1  | FAR2_PENMO  |
| 18         | 16    | 26.7        | 10     | 1  | TKL4_LOCOMI |
| 19         | 16    | 26.7        | 14     | 1  | ANGT_HORSE  |
| 20         | 16    | 26.7        | 14     | 1  | RS19_CLOPP  |
| 21         | 16    | 26.7        | 14     | 1  | RS19_LOMBP  |
| 22         | 15    | 25.0        | 8      | 1  | RS1_ERWCH   |
| 23         | 15    | 25.0        | 9      | 1  | ULAD_HUMAN  |
| 24         | 15    | 25.0        | 10     | 1  | TKN1_SCYCA  |
| 25         | 15    | 25.0        | 11     | 1  | CA42_LITCI  |
| 26         | 15    | 25.0        | 11     | 1  | TKC2_CALVO  |
| 27         | 15    | 25.0        | 13     | 1  | NPI_TYMST   |
| 28         | 15    | 25.0        | 13     | 1  | NP4_TYMST   |
| 29         | 15    | 25.0        | 13     | 1  | TEML_RANTE  |
| 30         | 15    | 25.0        | 14     | 1  | RS19_PWBMP  |
| 31         | 15    | 25.0        | 14     | 1  | SMS1_MYOSC  |
| 32         | 15    | 25.0        | 14     | 1  | SMS_ALIMI   |
| 33         | 14    | 23.3        | 9      | 1  | FAR4_CALVO  |

|    |    |      |    |   |            |
|----|----|------|----|---|------------|
| 34 | 14 | 23.3 | 9  | 1 | FIBB_PAPHA |
| 35 | 14 | 23.3 | 9  | 1 | HUTU_KUEAE |
| 36 | 14 | 23.3 | 10 | 1 | ANGT_BOVIN |
| 37 | 14 | 23.3 | 10 | 1 | PVK_LOCOMI |
| 38 | 14 | 23.3 | 10 | 1 | RL16_ACHLA |
| 39 | 14 | 23.3 | 10 | 1 | TRP8_LEUMA |
| 40 | 14 | 23.3 | 11 | 1 | TKN_PHYFU  |
| 41 | 14 | 23.3 | 12 | 1 | LICH_BACLI |
| 42 | 14 | 23.3 | 12 | 1 | XYLA_STRYN |
| 43 | 14 | 23.3 | 13 | 1 | IDHC_PIG   |
| 44 | 14 | 23.3 | 13 | 1 | NEUT_CAVFO |
| 45 | 14 | 23.3 | 14 | 1 | ADFA_TENMO |

ALIGNMENTS

| RESULT 1   |   |           |      |        |                    |
|--|---|-----------|------|--------|--------------------|
| ID   | TKNB_RANCA  | STANDARD; | PRT; | 10 AA. |                    |
| AC   | P22689;   |           |      |        | P19343 papio hamad |
| DT   | 01-AUG-1991 (Rel. 19, Created)  |           |      |        | P12381 klebsiella  |
| DT   | 01-AUG-1991 (Rel. 19, Last sequence update)   |           |      |        | P01017 bos taurus  |
| DT   | 10-OCT-2003 (Rel. 42, Last annotation update)   |           |      |        | P83382 locusta mig |
| DE   | Ranachykinin B (RTK B).   |           |      |        | P29221 acholepiasm |
| OS   | Rana catesbeiana (Bull frog).   |           |      |        | P81740 leucophaea  |
| OC   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |           |      |        | P08615 physalaemus |
| OC   | Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.   |           |      |        | P29297 bacillus li |
| OX   | NCBI_TaxID=8400;  |           |      |        | P14405 streptomyc  |
| RN   | [1]   |           |      |        | P20304 sus scrofa  |
| RP   | SEQUENCE, AND SYNTHESIS.  |           |      |        | P32560 cavia porce |
| RC   | TISSUE=Brain;   |           |      |        | P82965 tenebrio mo |
| RX   | MEDLINE=91254337; PubMed=2043143;   |           |      |        |                    |
| RA   | Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;   |           |      |        |                    |
| RT   | "Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.";  |           |      |        |                    |
| RL   | Regul. Pept. 46:81-88(1993).  |           |      |        |                    |
| CC   | -!- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secretagogues, and contract (directly or indirectly) many smooth muscles. |           |      |        |                    |
| CC   | -!- SUBCELLULAR LOCATION: Secreted.   |           |      |        |                    |
| CC   | -!- SIMILARITY: Belongs to the tachykinin family.   |           |      |        |                    |
| DR   | PIR; B61033; B61033.  |           |      |        |                    |
| DR   | InterPro; IPR002040; Tachy Neurokinin.  |           |      |        |                    |
| DR   | PROSITE; PS00267; TACHYKININ; 1.  |           |      |        |                    |
| KW   | Tachykinin; Neuropeptide; Amidation.  |           |      |        |                    |
| FT   | MOD_RES 10  |           |      |        |                    |
| FT   | MOD_RES 10  |           |      |        |                    |
| FT   | SEQUENCE 10 AA; 1210 MW; 917B556B59D5BAB5 CRC64;  |           |      |        |                    |
| Query Match  |   |           |      |        |                    |
| Best Local Similarity 42.9%; Score 21; DB 1; Length 10;    |   |           |      |        |                    |
| Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0; |   |           |      |        |                    |
| Oy   | 2 YKNSKPH 8   |           |      |        |                    |
| Db   | 1 YKSDSFY 7   |           |      |        |                    |
| RESULT 2   |   |           |      |        |                    |
| ID   | FAR7_PENMO  | STANDARD; | PRT; | 12 AA. |                    |
| AC   | P83322;   |           |      |        |                    |
| DT   | 28-FEB-2003 (Rel. 41, Created)  |           |      |        |                    |
| DT   | 28-FEB-2003 (Rel. 41, Last sequence update)   |           |      |        |                    |

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DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP7 (GYRKPFPNGSIF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkaset C., Longyant S.,
RA Chaitisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1381.4; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1383 MW; 31209192EF49D777 CRC64;

Query Match 33.3%; Score 20; DB 1; Length 12;
Best Local Similarity 37.5%; Pred. No. 5.7e+02;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKSKFH 8
DB 1 GYRKPFPN 8

RESULT 3
LMA1 LOCMI STANDARD; PRT; 13 AA.
ID LMA1 LOCMI
AC P38496;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Lom-AG-myotropin I (Accessory gland myotropin I).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Male accessory gland;
RX MEDLINE=91271087; PubMed=2052501;
RA Paemen L., Tips A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Lom-AG-myotropin: a novel myotropic peptide from the male accessory
RT glands of Locusta migratoria."
RL Peptides 12:7-10(1991).
CC -1- FUNCTION: The exact physiological function is still unknown. This
CC myotropic peptide is active on the oviduct and, to a lesser
CC extent, on the hindgut. Transferred from the male to the female
CC during copulation.
CC -1- TISSUE SPECIFICITY: Male accessory glands.
KW Neuropeptide; Amidation.
FT MOD RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1368 MW; DE1ACAF482EB72D CRC64;

Query Match 33.3%; Score 20; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 6.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYKN 4
DB 1 GPKN 4

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RESULT 4
COXG_RAT STANDARD; PRT; 8 AA.
ID COXG_RAT
AC P80430;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIb (EC 1.9.3.1) (AED) (Fragment).
GN COX6B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform."
RL Eur. J. Biochem. 230:235-241(1995).
CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport. This protein may be one of the
CC heme-binding subunits of the oxidase.
CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricyochrome
CC c + 2 H(2)O.
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase VIb family.
DR PIR; S65381; S65381.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1039 MW; 8101E9CA73AE456 CRC64;

Query Match 31.7%; Score 19; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FHR 9
DB 6 FHR 8

RESULT 5
FAR7_MACRS STANDARD; PRT; 10 AA.
ID FAR7_MACRS
AC P83280;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP7 (GYGDRNFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21107394; PubMed=11179812;
RA Sithigorngul P., Sarathongkum W., Longyant S., Panchan N.,
RA Sithigorngul W., Petsom A.;
RT "Three more novel FMRamide-like neuropeptide sequences from the
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii."
RL Peptides 22:191-197(2001).
CC -1- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1244 MW; 3CFE9C29C4540AA8 CRC64;

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Query Match 31.7%; Score 19; DB 1; Length 10;  
Best Local Similarity 44.4%; Pred. No. 7.3e+02;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYKNSKFHR 9  
| | | | |  
DB 1 GYGDENFLR 9

## RESULT 6

MY14\_EISFO STANDARD; PRT; 14 AA.  
ID MY14\_EISFO  
AC P46979;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Myoactive tetradecapeptide (ETP).  
OS Eiseinia foetida (Common branding worm) (Common dung-worm).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;  
OC Lumbricina; Lumbricidae; Eiseinia.  
OX NCBI\_TaxID=6396;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Gut;  
RX MEDLINE=96087879; PubMed=8532604;  
RA Ukena K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H.,  
RA Nomoto K.;  
RT "A novel gut tetradecapeptide isolated from the earthworm, Eiseinia  
foetida.";  
RL Peptides 16:995-999(1995).  
CC -!- FUNCTION: Has a stimulative effect on the contraction of gut  
muscles.  
CC -!- SIMILARITY: TO INSECTS ALLATOTROPIN.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 14 14 AMIDATION.  
SQ SEQUENCE 14 AA; 1478 MW; CC9ABEF941CD91AD CRC64;

Query Match 31.7%; Score 19; DB 1; Length 14;  
Best Local Similarity 30.0%; Pred. No. 1e+03;  
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYKNSKFHRV 10  
| | | | |  
DB 1 GPKDGAADRI 10

## RESULT 7

LCK6\_LEUMA STANDARD; PRT; 8 AA.  
ID LCK6\_LEUMA  
AC P19988;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Leucokinin VI (L-VI).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Head;  
RX MEDLINE=87052651; PubMed=2877794;  
RA Holman G.M., Cook B.J., Nachman R.J.;  
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:  
myotropic peptides of Leucophaea maderae.";  
RL Comp. Biochem. Physiol. 88C:27-30(1987).  
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile  
activity of cockroach prothodum (hindgut).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
DR PIR; JS0316.  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;

Query Match 30.0%; Score 18; DB 1; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SKFH 8  
| | | | |  
DB 2 SSFH 5

## RESULT 8

ASL1\_BACSE STANDARD; PRT; 11 AA.  
ID ASL1\_BACSE  
AC P83146;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).  
OS Bacteroides stercoris.  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=46506;  
RN [1]  
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.  
RC STRAIN=HJ-15;  
RX MEDLINE=21223019; PubMed=11322884;  
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;  
RT "Purification and characterization of acharan sulfate lyases, two  
novel heparinases, from Bacteroides stercoris HJ-15.";  
RL Eur. J. Biochem. 268:2635-2641(2001).  
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,  
heparin and heparan sulfate.  
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.  
CC Activated by reducing agents, such as DL-dithiothreitol and 2-  
mercaptoethanol.  
CC -!- SUBUNIT: Monomer.  
CC -!- PTM: The N-terminus is blocked.  
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is  
7.2 and optimum temperature 45 degrees Celsius.  
KW Lyase; Heparin-binding.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;

Query Match 30.0%; Score 18; DB 1; Length 11;  
Best Local Similarity 25.0%; Pred. No. 1.3e+03;  
Matches 2; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 YKNSKFHR 9  
| | | | |  
DB 4 YSGHNYHQ 11

## RESULT 9

CXL1\_CONMR STANDARD; PRT; 11 AA.  
ID CXL1\_CONMR  
AC P58807;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Lambda-conotoxin CMrVIA.  
OS Conus marmoreus (Marble cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=42752;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=20564325; PubMed=10988292;

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RA Balaji R.A., Ohnake A., Sato K., Gopalakrishnakone P., Kini R.M.,
RA Seow K.T., Bay B.-H.;
RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
RT pattern and protein folding. Isolation and characterization from the
RT venom of Conus marmoreus.";
RL J. Biol. Chem. 275:39516-39522(2000).
CC -1- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=1237.93; MW_ERR=0.21; METHOD=Electrospray.
CC -1- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
KW Neurotoxin; Toxin; Hydroxylation.
FT DISULFID 2 11
FT MOD RES 10 10 HYDROXYLATION.
SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match
Best Local Similarity 30.0%; Score 18; DB 1; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYK 3
   |||
Db 4 GYK 6

RESULT 10
CXL4_CONMR STANDARD; PRT; 13 AA.
ID CXL4_CONMR
AC P58610;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Lambda/chi-conotoxin MtrB (Chi-MtrB).
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Scrobocconcha; Hypsogastropoda;
OC Neogastropoda; Conidae; Conus.
OX NCBI_TaxID=42752;
RN [1]
RP SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.
RC TISSUE=Venom;
RX MEDLINE=21419681; PubMed=11528421;
RA Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,
RA Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,
RA Lewis R.J.;
RT "Two new classes of conopeptides inhibit the alpha1-adrenoceptor and
RT noradrenaline transporter.";
RL Nat. Neurosci. 4:902-907(2001).
CC -1- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- PTM: Exists in two forms, due to cis-trans isomerization at His-
CC 11-Hyp-12.
CC -1- MASS SPECTROMETRY: MW=1393.52; METHOD=Electrospray.
CC -1- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
DR PDB; 1IEO; 03-APR-02.
KW Neurotoxin; Toxin; Hydroxylation; 3D-structure.
FT DISULFID 4 13
FT MOD RES 12 12 HYDROXYLATION.
SQ SEQUENCE 13 AA; 1382 MW; 277AAC376EAD2B58 CRC64;

Query Match
Best Local Similarity 30.0%; Score 18; DB 1; Length 13;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYK 3
   |||
Db 6 GYK 8

RESULT 11
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FARP_CALSI STANDARD; PRT; 9 AA.
ID FARP_CALSI
AC P38455;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide.
OS Callinectes sapidus (Blue crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Callinectes.
OX NCBI_TaxID=6763;
RN [1]
RP SEQUENCE.
RX MEDLINE=92270479; PubMed=1815216;
RA Krajinak K.G.;
RT "The identification and structure-activity relations of a
RT cardioactive FMRFamide-related peptide from the blue crab Callinectes
RT sapidus.";
RL Peptides 12:1295-1302(1991).
CC -1- FUNCTION: Cardioactive peptide.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1159 MW; 134F0729D5A4045B CRC64;

Query Match
Best Local Similarity 28.3%; Score 17; DB 1; Length 9;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKNS 5
   |||
Db 1 GYKNS 5

RESULT 12
COXM_RAT STANDARD; PRT; 10 AA.
ID COXM_RAT
AC P80431;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIrb, mitochondrial (EC 1.9.3.1)
DE (Fragment).
GN COX7B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RX STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform.";
RL Bur. J. Biochem. 230:235-241(1995).
CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferrocyclochrome
CC c + 2 H(2)O.
DR PIR; S65387; S65387.
KW Oxidoreductase; Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1210 MW; CFCT0EB771A33326 CRC64;

Query Match
Best Local Similarity 28.3%; Score 17; DB 1; Length 10;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 3 KNSKPH 8  
| | |  
Db 5 KPTPFH 10

## RESULT 13

EFQ\_CLOPA STANDARD; PRT; 11 AA.  
AC P81350;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Elongation factor G (EF-G) (CP 5) (Fragment).  
GN FUSA.  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1501;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W5;  
RX MEDLINE=98291870; PubMed=9629918;  
RA Flengsrud R., Skjeldal L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal  
sequence analysis of proteins from Clostridium pasteurianum W5.";  
RL Electrophoresis 19:802-806(1998).  
CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of  
the nascent protein chain from the A-site to the P-site of the  
ribosome.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.  
CC EF-G/EF-2 subfamily.  
DR InterPro; IPR000795; EF\_GRPbind.  
DR PROSITE; PS00301; EFACOR\_GTP; PARTIAL.  
KM Elongation factor; Protein biosynthesis; GTP-binding.  
FT NON TER 11  
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C3B17 CRC64;  
  
Query Match 28.3%; Score 17; DB 1; Length 11;  
Best Local Similarity 33.3%; Pred. No. 1.9e+03;  
Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 YKNSKPHRV 10  
| | |  
Db 2 YPLEKFCNT 10

RESULT 14  
NXSN PSETE STANDARD; PRT; 11 AA.  
AC P59072;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Short neurotoxin M1 (Alpha neurotoxin) (Fragment).  
OS Pseudonaja textilis (Eastern brown snake).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Elapidae; Acanthophiinae; Pseudonaja.  
OX NCBI\_TaxID=8673;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=99449602; PubMed=10518793;  
RA Gong N.L., Armugam A., Jeyaseelan K.;  
RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA  
cloning, expression and protein characterization.";  
RT Eur. J. Biochem. 265:982-989(1999).  
RL Eur. J. Biochem. 265:982-989(1999).  
CC -1- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic  
acetylcholine receptors (nAChR).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.  
CC -1- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.

CC -1- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.  
CC -1- SIMILARITY: Belongs to the snake toxin family.  
DR InterPro; IPR003571; Snake toxin.  
DR PROSITE; PS00272; SNAKE\_TOXIN; PARTIAL.  
KM Toxin; Neurotoxin; Postsynaptic neurotoxin;  
KW Acetylcholine receptor inhibitor; Multigene family.  
FT UNSURE 3  
FT NON TER 3  
SQ SEQUENCE 11 AA; 1319 MW; 0D1EFC81B58732B CRC64;

Query Match 28.3%; Score 17; DB 1; Length 11;  
Best Local Similarity 40.0%; Pred. No. 1.9e+03;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYKNS 5  
| | |  
Db 6 GYRDT 10

## RESULT 15

MY14\_PHEVI STANDARD; PRT; 14 AA.  
AC P46980;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Myoactive tetradecapeptide (PTP).  
OS Pheretima vittata (Earthworm).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;  
OC Lumbricina; Megascotolecidae; Pheretima.  
OX NCBI\_TaxID=46674;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Gut;  
RX MEDLINE=96087879; PubMed=8532604;  
RA Ukena K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H.,  
RA Nomoto K.;  
RT "A novel gut tetradecapeptide isolated from the earthworm, Eisenia  
foetida.";  
RL Peptides 16:995-999(1995).  
CC -1- FUNCTION: Has a stimulative effect on the contraction of gut  
muscles.  
CC -1- SIMILARITY: TO INSECTS ALLATOTROPIN.  
CC Neuropeptide; Amidation.  
KM MOD RES 14  
FT MOD RES 14  
SQ SEQUENCE 14 AA; 1522 MW; DA40BEE67CCD91AD CRC64;  
  
Query Match 28.3%; Score 17; DB 1; Length 14;  
Best Local Similarity 20.0%; Pred. No. 2.5e+03;  
Matches 2; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYKNSKPHRV 10  
| | |  
Db 1 GPRDGSADRI 10

RESULT 16  
LCK4\_LEUMA STANDARD; PRT; 8 AA.  
AC P21143;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Leucokinin IV (L-IV).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Head;  
RA Holman G.M., Cook B.J., Nachman R.J.;

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RN "Primary structure and synthesis of two additional neuropeptides
RT from leucophaea maderae: members of a new family of
RC Cephalomyotroptins."
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach proctoderm (hindgut).
CC -1- SUBCELLULAR LOCATION: Secreted.
KW Neuropeptide; Amidation.
SQ MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BD4 CRC64;

Query Match 26.7%; Score 16; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSKFF 8
Db 1 DASFF 5

RESULT 17
FAR2_PENMO STANDARD; PRT; 10 AA.
ID FAR2_PENMO STANDARD; PRT; 10 AA.
AC P83317;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE FMRamide-like neuropeptide FLIP2 (AYSNTLYLR-amide).
OS Pennaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Pennaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigornkul P., Pupuem J., Krungkassam C., Longyant S.,
RA Chaisituthangkura P., Sithigornkul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Pennaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1260.0; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1260 MW; 88F9023B54472455 CRC64;

Query Match 26.7%; Score 16; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 YKNSKFFHR 9
Db 2 YSNLNYLR 9

RESULT 18
TKL4_LOCM1 STANDARD; PRT; 10 AA.
ID TKL4_LOCM1 STANDARD; PRT; 10 AA.
AC P30250;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin IV (TK-IV).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
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RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91219696; PubMed=2132575;
RA Schoofs L., Holman G.M., Hayes T.K., Kochansky J.P., Nachman R.J.,
RA de Loof A.;
RT "Locustatachykinin III and IV: two additional insect neuropeptides
RT with homology to peptides of the vertebrate tachykinin family."
RL Regul. Pept. 31:199-212(1990).
CC -1- FUNCTION: Myoactive peptide. Stimulates the contraction of the
CC oviduct and foregut.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
DR PIR; B60073; ECLQ4M.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1040 MW; 9E52CD71E9C8735 CRC64;

Query Match 26.7%; Score 16; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FHRV 10
Db 6 FHGV 9

RESULT 19
ANGT_HORSE STANDARD; PRT; 14 AA.
ID ANGT_HORSE STANDARD; PRT; 14 AA.
AC P01016;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang
DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
DE (Fragment).
GN AGT OR SERPIN8.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
RT "The preparation, purification, and amino acid sequence of a
RT polypeptide renin substrate."
RL J. Exp. Med. 106:439-453(1957).
CC -1- FUNCTION: In response to lowered blood pressure, the enzyme renin
CC cleaves angiotensin I, from angiotensinogen. ACE (angiotensin
CC converting enzyme) then removes a dipeptide to yield the
CC physiologically active peptide angiotensin II, the most potent
CC pressor substance known, which helps regulate volume and mineral
CC balance of body fluids.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- SIMILARITY: Belongs to the serpin family.
DR PIR; A92775; A01250.
DR PDB; 1ER8; 15-OCT-91.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT NON TER 2 8 ANGIOTENSIN III.
FT SEQUENCE 14 AA; 1759 MW; 2E9921F8EEFBDD7 CRC64;

Query Match 26.7%; Score 16; DB 1; Length 14;
Best Local Similarity 40.0%; Pred. No. 3.9e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 FHRVI 11
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Db 8 FHLV 12

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RESULT 20
RS19_CLOPP STANDARD; PRT; 14 AA.
AC Q46228;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS19.
OS Clover proliferation phytolasma.
OC Bacteria; Firmicutes; Mollicutes; Acholoplasmatales;
OC Acholoplasmataceae; Phytolasma.
OX NCBI_TaxID=35776;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
RT their classification."
RL J. Bacteriol. 176:5244-5254(1994).
CC -1- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
CC to the 16S ribosomal RNA (By similarity).
CC -1- SIMILARITY: Belongs to the S19p family of ribosomal proteins.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL: L27011; AAA83938.1; -.
DR HAMAP; MF_00531; -.
DR InterPro; IPR002222; Ribosomal_S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1642 MW; 20C478EB9FFFE4A8 CRC64;

Query Match 26.7%; Score 16; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSK 6
Db 10 KNQK 13

RESULT 21
RS19_LOWBP STANDARD; PRT; 14 AA.
AC Q48878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS19.
OS Locofah witches'-broom phytolasma.
OC Bacteria; Firmicutes; Mollicutes; Acholoplasmatales;
OC Acholoplasmataceae; Phytolasma.
OX NCBI_TaxID=35773;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
RT their classification."
RL J. Bacteriol. 176:5244-5254(1994).

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CC -1- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
CC to the 16S ribosomal RNA (By similarity).
CC -1- SIMILARITY: Belongs to the S19p family of ribosomal proteins.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL: L27027; AAA83944.1; -.
DR HAMAP; MF_00531; -.
DR InterPro; IPR002222; Ribosomal_S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1642 MW; 20C478EB9FFFE4A8 CRC64;

Query Match 26.7%; Score 16; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSK 6
Db 10 KNQK 13

RESULT 22
RS1_ERWCH STANDARD; PRT; 8 AA.
AC P37985;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 30S ribosomal protein S1 (Fragment).
GN RPSA.
OS Erwinia chrysanthemi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3937;
RA Douille A., Toussaint A., Faellen M.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BINDS MRNA; THUS FACILITATING RECOGNITION OF THE
CC INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT
CC SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the S1P family of ribosomal proteins.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL: X74750; CAA52769.1; -.
DR PIR; S37141; S37141.
KW Ribosomal protein; Repeat; RNA-binding.
FT NON_TER 1
SQ SEQUENCE 8 AA; 837 MW; 9E18733DC5B339CD CRC64;

Query Match 25.0%; Score 15; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKNSK 6
Db 2 FKSAK 6

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RESULT 23  
 TLAD\_HUMAN STANDARD; PRT; 9 AA.  
 ID TLAD\_HUMAN  
 AC P31929;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=94147969; PubMed=8313870;  
 RA Hughes G.J., Frutiger S., Paquet N., Pasquai C., Sanchez J.-C.,  
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;  
 RT "Human liver protein map: update 1993."  
 RL Electrophoresis 14:1216-1222(1993).  
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 6, its MW is: 15 kDa.  
 DR SWISS-2DPAGE; P31929; HUMAN.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1129 MW; D02DFB41B6D3322 CRC64;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RA "Caerulein-like peptides from the skin glands of the Australian blue  
 RT mountain tree frog *Litoria citropa*. Part 1. Sequence determination  
 RT using electrospray mass spectrometry."  
 RT Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 CC -1- FUNCTION: Hypotensive neuropeptide (Probable).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -1- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being  
 CC sulfated.  
 CC -1- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.  
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro: IPR001651; Gastrin.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 1 4  
 FT MOD\_RES 4 4  
 FT MOD\_RES 11 11  
 FT MOD\_RES 11 11  
 SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=86192829; PubMed=2422058;  
 RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.;  
 RA "Scyliorhinin I and II: two novel tachykinins from dogfish gut."  
 RT FEBS Lett. 200:111-116(1986).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=93292508; PubMed=7685693;  
 RA Waugh D., Wang Y., Hazon N., Balmert R.J., Conlon J.M.;  
 RA "Primary structures and biological activities of substance-P-related  
 RT peptides from the brain of the dogfish, *Scyliorhinus canicula*."  
 RL Eur. J. Biochem. 214:469-474(1993).  
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; A24867; A24867.  
 DR InterPro: IPR002040; Tachy\_Neurokinin.

DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10  
 SQ SEQUENCE 10 AA; 1219 MW; D0602D6B59C33AA9 CRC64;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RA "Caerulein-like peptides from the skin glands of the Australian blue  
 RT mountain tree frog *Litoria citropa*. Part 1. Sequence determination  
 RT using electrospray mass spectrometry."  
 RT Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 CC -1- FUNCTION: Hypotensive neuropeptide (Probable).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -1- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being  
 CC sulfated.  
 CC -1- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.  
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro: IPR001651; Gastrin.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 1 4  
 FT MOD\_RES 4 4  
 FT MOD\_RES 11 11  
 FT MOD\_RES 11 11  
 SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=86192829; PubMed=2422058;  
 RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.;  
 RA "Scyliorhinin I and II: two novel tachykinins from dogfish gut."  
 RT FEBS Lett. 200:111-116(1986).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=93292508; PubMed=7685693;  
 RA Waugh D., Wang Y., Hazon N., Balmert R.J., Conlon J.M.;  
 RA "Primary structures and biological activities of substance-P-related  
 RT peptides from the brain of the dogfish, *Scyliorhinus canicula*."  
 RL Eur. J. Biochem. 214:469-474(1993).  
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; A24867; A24867.  
 DR InterPro: IPR002040; Tachy\_Neurokinin.

OX NCB1\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=95075727; PubMed=7984492;  
 RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,  
 RA Naessel D.R.;  
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from  
 RT the blowfly, Calliphora vomitoria, that have resemblances to  
 RT tachykinins.";  
 RL Peptides 15:761-768(1994).  
 CC -1- FUNCTION: Myoactive peptide.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD RES 11 11  
 SQ SEQUENCE 11 AA; 1103 MW; 15D7B3F9C9CDD444 CRC64;

Query Match 25.0%; Score 15; DB 1; Length 11;  
 Best Local Similarity 42.9%; Pred. No. 4.6e+03;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 GYKNSKF 7  
 DB 1 GLGNNAF 7

## RESULT 27

NP1\_LYMST STANDARD; PRT; 13 AA.  
 ID NP1\_LYMST  
 AC P80178;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Lymnaea-Df-amide 1.  
 OS Lymnaea stagnalis (Great pond snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
 OC Lymnaeidae; Lymnaeidae; Lymnaea.  
 OX NCB1\_TaxID=6523;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Ganglion;  
 RX MEDLINE=93238777; PubMed=8477756;  
 RA Johnsen A.H., Rehfeld J.F.;  
 RT "Lymnaeidae, a new family of neuropeptides from the pond snail,  
 RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in  
 RT invertebrates?";  
 RL Eur. J. Biochem. 213:875-879(1993).  
 CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.  
 DR PIR: S32471; S32471.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 13 13  
 SQ SEQUENCE 13 AA; 1519 MW; 9CA07BA3F5D5B455 CRC64;

Query Match 25.0%; Score 15; DB 1; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 NSKF 7  
 DB 7 NSAF 10

## RESULT 28

NP4\_LYMST STANDARD; PRT; 13 AA.  
 ID NP4\_LYMST  
 AC P80181;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Lymnaea-Df-amide 4.  
 OS Lymnaea stagnalis (Great pond snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
 OC Lymnaeidae; Lymnaeidae; Lymnaea.

OX NCB1\_TaxID=6523;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Ganglion;  
 RX MEDLINE=93238777; PubMed=8477756;  
 RA Johnsen A.H., Rehfeld J.F.;  
 RT "Lymnaeidae, a new family of neuropeptides from the pond snail,  
 RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in  
 RT invertebrates?";  
 RL Eur. J. Biochem. 213:875-879(1993).  
 CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.  
 DR PIR: S32474; S32474.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 13 13  
 SQ SEQUENCE 13 AA; 1503 MW; 9CA07BB56D5B455 CRC64;

Query Match 25.0%; Score 15; DB 1; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 NSKF 7  
 DB 7 NSAF 10

## RESULT 29

TEML\_PANTE STANDARD; PRT; 13 AA.  
 ID TEML\_PANTE  
 AC P57104;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Temporin L.  
 OS Rana temporaria (European common frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.  
 OX NCB1\_TaxID=8407;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=97175050; PubMed=9022710;  
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,  
 RA Barra D.;  
 RT "Temporins, antimicrobial peptides from the European red frog Rana  
 RT temporaria.";  
 RL Eur. J. Biochem. 242:788-792(1996).  
 CC -1- FUNCTION: Has antibacterial activity against Gram-negative and  
 CC Gram-positive bacteria.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- SIMILARITY: Belongs to the brevinin family.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT MOD RES 13 13  
 SQ SEQUENCE 13 AA; 1641 MW; 9EBDCB1FAFF7C325 CRC64;

Query Match 25.0%; Score 15; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SKF 7  
 DB 6 SKF 8

## RESULT 30

RS19\_PPWPB STANDARD; PRT; 14 AA.  
 ID RS19\_PPWPB  
 AC Q52093;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 30S ribosomal protein S19 (Fragment).  
 GN RPSS OR RPS19.

OS Pigeon pea witches'-broom phytoplasma.  
OC Bacteria; Firmicutes; Mollicutes; Achaeleplasmatales;  
OC Achaeleplasmataceae; Phytoplasma.  
OX NCBI\_TaxID=37700;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94350802; PubMed=8071198;  
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;  
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for  
their classification."  
RL J. Bacteriol. 176:5244-5254(1994).  
CC -1- FUNCTION: Protein S19 forms a complex with S13 that binds strongly  
to the 16S ribosomal RNA (By similarity).  
CC -1- SIMILARITY: Belongs to the S19p family of ribosomal proteins.  
CC -----  
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CC -----  
DR EMBL; L27036; AAA83946.1; -.  
DR HAMAP; MF\_00531; -; 1.  
DR InterPro; IPR002222; Ribosomal\_S19.  
DR PROSITE; PS00323; RIBOSOMAL\_S19; PARTIAL.  
KW Ribosomal protein; rRNA-binding.  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1668 MW; 8FD46FB830DFBBA CRC64;  
  
Query Match 25.0%; Score 15; DB 1; Length 14;  
Best Local Similarity 75.0%; Pred. No. 6e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 KNSK 6  
|:|  
Db 6 KDSK 9  
  
RESULT 31  
SMS1\_MYOSC  
ID SMS1\_MYOSC STANDARD; PRT; 14 AA.  
AC P20750;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Somatostatin I.  
OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin),  
OS Oncorhynchus kisutch (Coho salmon), and  
OS Anguilla anguilla (European freshwater eel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;  
OC Cottidae; Cottidae; Myoxocephalus.  
OX NCBI\_TaxID=8097, 8019, 7936;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=M.scorpius; TISSUE=Pancreas;  
RX MEDLINE=88029486; PubMed=2889597;  
RA Conlon J.M., Davis M.S., Falkner S., Thim L.;  
RT "Structural characterization of peptides derived from  
prosomatostatin I and II isolated from the pancreatic islets of two  
species of teleostean fish: the daddy sculpin and the flounder."  
RL Eur. J. Biochem. 168:647-652(1987).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=O.kisutch; TISSUE=Pancreas;  
RX MEDLINE=87055212; PubMed=2877919;  
RA Plisevskaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,  
RA Kimmel J.R., Andrews P.C., Gorman A.;  
RT "Characterization of coho salmon (Oncorhynchus kisutch) islet  
somatostatins.";

RL Gen. Comp. Endocrinol. 63:252-263(1986).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=A.anguilla; TISSUE=Pancreas;  
RX MEDLINE=89065329; PubMed=2904391;  
RA Conlon J.M., Deacon C.F., Hazon N., Henderson I.W., Thim L.;  
RT "Somatostatin-related and glucagon-related peptides with unusual  
structural features from the European eel (Anguilla anguilla).";  
RL Gen. Comp. Endocrinol. 72:181-189(1988).  
CC -1- FUNCTION: Somatostatin inhibits the release of somatotropin.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the somatostatin family.  
DR PIR; A60840; A60840.  
DR PIR; B60842; B60842.  
DR PIR; S00172; S00172.  
DR InterPro; IPR004250; Somatostatin.  
DR Pfam; PF03002; Somatostatin; 1.  
KW Hormone; Multigene family.  
FT DISULFID 3  
SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;  
  
Query Match 25.0%; Score 15; DB 1; Length 14;  
Best Local Similarity 75.0%; Pred. No. 6e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GYKN 4  
|:|  
Db 2 GCKN 5  
  
RESULT 32  
SMS\_ALIMI  
ID SMS\_ALIMI STANDARD; PRT; 14 AA.  
AC P31885;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Somatostatin-14.  
OS Alligator mississippiensis (American alligator), and  
OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
OX NCBI\_TaxID=8496, 34903;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=A.mississippiensis; TISSUE=Stomach;  
RX MEDLINE=93324451; PubMed=8101369;  
RA Wang Y., Conlon J.M.;  
RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain  
and stomach of the alligator.";  
RL Peptides 14:573-579(1993).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=T.scripta;  
RX MEDLINE=90341082; PubMed=1974347;  
RA Conlon J.M., Hicks J.W.;  
RT "Isolation and structural characterization of insulin, glucagon and  
somatostatin from the turtle, Pseudemys scripta.";  
RL Peptides 11:461-466(1990).  
CC -1- FUNCTION: Somatostatin inhibits the release of somatotropin.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the somatostatin family.  
DR PIR; C60414; C60414.  
DR InterPro; IPR004250; Somatostatin.  
DR Pfam; PF03002; Somatostatin; 1.  
KW Hormone.  
FT DISULFID 3  
SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;  
  
Query Match 25.0%; Score 15; DB 1; Length 14;  
Best Local Similarity 75.0%; Pred. No. 6e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKN 4  
| | |  
Db 2 GCKN 5

## RESULT 33

FAR4\_CALVO STANDARD; PRT; 9 AA.  
AC P41859;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CalliFMRamide 4.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCB1\_TaxID=27454;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Thoracic ganglion;  
RX MEDLINE=9219611; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated calliFMRamides) from the blowfly  
RT Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
CC family.  
DR PIR; D41978; D41978.  
KW Neuropeptide; Amidation.  
FT MOD RES 9  
SQ SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NSKFRH 9  
| | |  
Db 3 NQDFMR 8

## RESULT 34

FIBB\_PAPHA STANDARD; PRT; 9 AA.  
AC P19343;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
GN FGB.  
OS Papio hamadryas (Hamadryas baboon).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Papio.  
OX NCB1\_TaxID=9557;  
RN [1]  
RP SEQUENCE.

RX MEDLINE=84161822; PubMed=6423621;  
RA Nakamura S., Takenaka O., Takahashi K.;  
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,  
RT and Theropithecus gelada): their amino acid sequences and  
RT evolutionary rates and a molecular phylogeny for the baboons.";  
RL J. Biochem. 94:1973-1978(1983).  
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that  
CC polymerize into fibrin and acting as a cofactor in platelet  
CC aggregation.  
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,  
CC which cleaves fibrinopeptides A and B from alpha and beta chains,

CC and thus exposes the N-terminal polymerization sites responsible  
CC for the formation of the soft clot.  
DR PIR; E28854; E28854.  
DR InterPro; IPR002181; Fibrinogen\_C.  
DR PROSITE; PS00514; FIBRIN\_AG\_C\_DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma.  
FT PEPTIDE 1  
FT NON TER 9  
SQ SEQUENCE 9 AA; 1057 MW; DDFE71E9C7287B06 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FH 8  
| |  
Db 6 FH 7

## RESULT 35

HUTU\_KLEAE STANDARD; PRT; 9 AA.  
AC P12381;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Urocanate hydratase (EC 4.2.1.49) (Urocanase) (Imidazolonepropionate  
DE hydrolase) (Fragment).  
GN HUTU.  
OS Klebsiella aerogenes.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCB1\_TaxID=28451;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8198018; PubMed=2834335;  
RA Nieuwkoop A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;  
RT "Bidirectional promoter in the hut(p) region of the histidine  
RT utilization (hut) operons from Klebsiella aerogenes.";  
RL J. Bacteriol. 170:2240-2246(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9036861; PubMed=2203754;  
RA Schwacha A., Bender R.A.;

RT "Nucleotide sequence of the gene encoding the repressor for the  
RT histidine utilization genes of Klebsiella aerogenes.";  
RL J. Bacteriol. 172:5477-5481(1990).  
CC -1- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-  
CC y1)propanoate = urocanate + H(2)O.  
CC -1- COFACTOR: Binds 1 NAD per subunit (By similarity).  
CC -1- PATHWAY: Histidine degradation; second step.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: Belongs to the urocanase family.

CC -----  
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CC -----  
DR EMBL; M19665; AAA25078.1; -.  
DR EMBL; M34604; AAA25076.1; -.  
DR HAMAP; MF\_00577; -; 1.  
DR InterPro; IPR000193; Urocanase.  
DR PROSITE; PS01233; UROCANASE; PARTIAL.  
KW Histidine metabolism; Lyase; NAD.  
FT NON TER 9  
SQ SEQUENCE 9 AA; 1140 MW; 970FC41B5325A6C5 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 9;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;

Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SKFHRV 10  
| | : : :  
Db 4 SKYRQL 9

RESULT 36

ANGT\_BOVIN STANDARD; PRT; 10 AA.  
ID ANGT\_BOVIN  
AC P01017;  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]  
DE (Fragment).  
GN AGT OR SERPINA8.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
OC Bovidae; Bovinae; Bos.  
CX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RA Elliott D.F., Peart W.S.;  
RT "The amino acid sequence in a hypertensin.";  
RL Biochem. J. 65:246-254(1957).  
CC -1- FUNCTION: In response to lowered blood pressure, the enzyme renin cleaves angiotensin I, from angiotensinogen. ACE (angiotensin converting enzyme) then removes a dipeptide to yield the physiologically active peptide angiotensin II, the most potent pressor substance known, which helps regulate volume and mineral balance of body fluids.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.  
CC -1- SIMILARITY: Belongs to the serpin family.  
DR PIR; A90345; A90345.  
DR PDB; 3ER5; 15-JUL-92.  
DR InterPro; IPR000215; Serpin.  
DR PROSITE; PS00284; SERPIN; PARTIAL.  
KW Vasconstrictor; Plasma; Serpin; 3D-structure.  
FT PEPTIDE 1 10 ANGIOTENSIN I.  
FT PEPTIDE 1 8 ANGIOTENSIN II.  
FT PEPTIDE 2 8 ANGIOTENSIN III.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1282 MW; CEEFBD761F2D842 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FH 8  
| |  
Db 8 FH 9

RESULT 37

PVK\_LOCM1 STANDARD; PRT; 10 AA.  
ID PVK\_LOCM1  
AC P83382;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Periviscerokinin (Lom-PVK-1).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Abdominal perisymphathetic organs;

RX MEDLINE=21896327; PubMed=11897380;  
RA Predel R., Gaede G.;  
RT "Identification of the abundant neuropeptide from abdominal perisymphathetic organs of locusts.";  
RL Peptides 23:621-627(2002).  
CC -1- FUNCTION: Myotropic peptide; increases the frequency of contraction of the heart and stimulates amplitude and tonus of the foregut.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- MASS SPECTROMETRY: MW=1104.5; METHOD=MALDI.  
DR GO; GO:0005576; C:extracellular; IDA.  
DR GO; GO:0005184; F:neuropeptide hormone activity; IDA.  
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.  
KW Neuropeptide; Amidation.  
FT MOD RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1105 MW; 39811269D6D9C728 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 10;  
Best Local Similarity 60.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 KFHVR 10  
| | : : :  
Db 6 QFPRV 10

RESULT 38

RL16\_ACHLA STANDARD; PRT; 10 AA.  
ID RL16\_ACHLA  
AC P29221;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE 50S ribosomal protein L16 (Fragment).  
GN RPLP.  
OS Acholeplasma laidlawi.  
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales; Acholeplasmataceae; Acholeplasma.  
OX NCBI\_TaxID=2148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92210505; PubMed=1556079;  
RA Lim P.O., Sears B.B.;  
RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like organism and Acholeplasma laidlawi deduced from two ribosomal protein gene sequences.";  
RT J. Bacteriol. 174:2606-2611(1992).  
RL -1- FUNCTION: This protein binds directly to 23S ribosomal RNA and is located at the site of the peptidyltransferase center (By similarity).  
CC -1- SIMILARITY: Belongs to the L16P family of ribosomal proteins.

-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL; M74771; AAA21914.1; -.  
DR PIR; F41839; F41839.  
DR InterPro; IPR000114; Ribosomal L16.  
DR PROSITE; PS00586; RIBOSOMAL\_L16\_1; PARTIAL.  
DR PROSITE; PS00701; RIBOSOMAL\_L16\_2; PARTIAL.  
KW Ribosomal protein; rRNA-binding.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1324 MW; B3386A21B4032766 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;



QY 3 KNSKF 7  
| : | :  
Db 5 KRTKY 9

## RESULT 39

TRP8\_LEUMA STANDARD; PRT; 10 AA.

AC P81740;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tachykinin-related peptide 8 (LentRP 8).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]

## SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Brain;  
RX MEDLINE=97269266; PubMed=9114447;  
RA Muren J.E., Naessel D.R.;  
RT "Seven tachykinin-related peptides isolated from the brain of the  
RT Madeira cockroach; evidence for tissue-specific expression of  
RT isoforms."  
RL Peptides 18:7-15(1997).

CC -1- FUNCTION: Myoactive peptide. Increases the amplitude and frequency  
CC of spontaneous contractions and tonus of hindgut muscle.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Brain.

CC -1- MASS SPECTROMETRY: MW=1076.9; METHOD=MALDI.

CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.

KW Tachykinin; Neuropeptide; Amidation.

FT MOD\_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1076 MW; 9E410371E9C87685 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FH 8  
| : | :  
Db 6 FH 7

## RESULT 40

TKN\_PHYFU STANDARD; PRT; 11 AA.

AC P08615;  
DT 01-AUG-1988 (Rel. 08, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Physalaemin.

OS Physalaemus fuscumaculatus (Neotropical frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Leptodactylidae;

OC Leptodactylinae; Physalaemus.

OX NCBI\_TaxID=8378;  
RN [1]

## SEQUENCE.

RP TISSUE=Skin secretion;

RX MEDLINE=66076612; PubMed=5857249;

RA Erspamer V., Anastasi A., Bertaccini G., Cel J.M.;

RT "Structure and pharmacological actions of Physalaemin, the main

RT active polypeptide of the skin of Physalaemus fuscumaculatus.";

RL Experientia 20:489-490(1964).

CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,

CC evoke behavioral responses, are potent vasodilators and

CC secretagogues, and contract (directly or indirectly) many smooth

CC muscles.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Skin.

CC -1- SIMILARITY: Belongs to the tachykinin family.

DR PIR; S07201; S07201.

DR InterPro; IPR002040; Tachy Neurokinin.

DR Pfam; PF02202; Tachykinin\_1.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;

KW Pyroglutamate carboxylic acid.

FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.

FT MOD\_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 11;  
Best Local Similarity 50.0%; Pred. No. 7.1e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SKFH 8  
| : | :  
Db 5 NKFY 8

## RESULT 41

LICH\_BACLI STANDARD; PRT; 12 AA.

AC P82907;  
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Lichenin.

OS Bacillus licheniformis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_TaxID=1402;  
RN [1]

## SEQUENCE.

RC STRAIN=26L-10/3RA;

RX MEDLINE=21460732; PubMed=11576300;

RA Pattnaik P., Kaushik J.K., Grover S., Batish V.K.;

RT "Purification and characterization of a bacteriocin-like compound

RT (Lichenin) produced anaerobically by Bacillus licheniformis isolated

RT from water buffalo.";

RT J. Appl. Microbiol. 91:636-645(2001).

RN [2]

## SEQUENCE.

RC STRAIN=26L-10/3RA;

RA Pattnaik P.;

RT "Biochemical characterization and molecular genetics of bacteriocin

RT produced by a selected rumen bacterial isolate.";

RT Thesis (1999), National Dairy Research Institute / Karnal, India.

CC -1- FUNCTION: OXYGEN LABILE BACTERIOCIN-LIKE. HAS ANTIBACTERIAL

CC ACTIVITY.

CC -1- SUBCELLULAR LOCATION: Secreted.

KW Antibiotic; Bacteriocin.

SQ SEQUENCE 12 AA; 1414 MW; 1C059B6CED4AEEB0 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FH 8  
| : | :  
Db 9 FH 10

## RESULT 42

XYLA\_STRVN STANDARD; PRT; 12 AA.

AC P14405;  
DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Xylose isomerase (EC 5.3.1.5) (Fragment).

XYLA.

OS Streptomyces violaceoruber.

CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

CC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1935;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=LMG 7183;  
 RX MEDLINE=90104230; PubMed=2604694;  
 RA Vangyysperre W., Ampe C., Kersters-Hilderson H., Tempst P.;  
 RT "Single active-site histidine in D-xylose isomerase from Streptomyces  
 violaceoruber. Identification by chemical derivatization and peptide  
 mapping.";  
 RL Biochem. J. 263:195-199(1989).  
 CC -1- CATALYTIC ACTIVITY: D-xylose = D-xylose.  
 CC -1- COFACTOR: Binds 2 magnesium ions per subunit (Potential).  
 CC -1- SUBUNIT: Homotetramer.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to the xylose isomerase family.  
 DR HAMAP; MF\_00455; -; 1.  
 DR InterPro; IPR001998; Xylose\_isom.  
 DR PROSITE; PS00172; XYLOSE\_ISOMERASE\_1; PARTIAL.  
 DR PROSITE; PS00173; XYLOSE\_ISOMERASE\_2; PARTIAL.  
 KW Isomerase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium.  
 FT NON\_TER 1 1  
 FT ACT\_SITE 5 5  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1375 MW; E749268EB1AAAA1 CRC64;  
 Query Match 23.3%; Score 14; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 FH 8  
 Db 4 FH 5  
 RESULT 43  
 IDHC\_PIG STANDARD; PRT; 13 AA.  
 AC P20304;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1.1.1.42)  
 DE (Oxalosuccinate decarboxylase) (IDH) (NADP+-specific IDH) (IDP)  
 DE (Fragment).  
 GN IDH1.  
 OS Sus scrofa (Pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=87308293; PubMed=2887570;  
 RA Bailey J.M., Colman R.F.;  
 RT "Isolation of the glutamyl peptide labeled by the nucleotide analogue  
 2-(4-bromo-2,3-dioxobutylthio)-1,N(6)-ethenadenosine  
 2',5'-biphosphate in the active site of NADP+-specific isocitrate  
 dehydrogenase.";  
 RL J. Biol. Chem. 262:12620-12626(1987).  
 RN [2]  
 RP SEQUENCE.  
 RX MEDLINE=87308292; PubMed=3624273;  
 RA Ehrlich R.S., Colman R.F.;  
 RT "Characterization of an active site peptide modified by the substrate  
 analogue 3-bromo-2-ketoglutarate on a single chain of dimeric NADP+-  
 dependent isocitrate dehydrogenase.";  
 RL J. Biol. Chem. 262:12614-12619(1987).  
 CC -1- CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2)  
 CC + NADPH.  
 CC -1- SUBUNIT: Homodimer.  
 DR InterPro; IPR001804; Isodh.  
 DR PROSITE; PS00470; IDH\_IMDH; PARTIAL.  
 KW Oxidoreductase; NADP; Tricarboxylic acid cycle.

FT NON\_TER 1 1  
 FT ACT\_SITE 5 5  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1353 MW; 1B640F0E9F7C71E0 CRC64;  
 Query Match 23.3%; Score 14; DB 1; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GYNSK 6  
 Db 8 GLSNVK 13  
 RESULT 44  
 NEUT\_CAVPO STANDARD; PRT; 13 AA.  
 ID NEUT\_CAVPO  
 AC P32560;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neurotensin (NT).  
 GN NTS.  
 OS Cavia porcellus (Guinea pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE.  
 RX TISSUE=Small intestine;  
 RC MEDLINE=86248085; PubMed=3087775;  
 RA Shaw C., Thim L., Conlon J.M.;  
 RT "[Ser7]neurotensin: isolation from guinea pig intestine.";  
 RL FEBS Lett. 202:187-192(1986).  
 CC -1- FUNCTION: Smooth muscle-contracting peptide.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the neurotensin family.  
 DR PIR; A53608; A53608.  
 KW Vasoactive; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1  
 FT SEQUENCE 13 AA; 1680 MW; 4C8314644C4115B3 CRC64;  
 SQ  
 Query Match 23.3%; Score 14; DB 1; Length 13;  
 Best Local Similarity 66.7%; Pred. No. 8.5e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 YKN 4  
 Db 3 YEN 5  
 RESULT 45  
 ADFA\_TENMO STANDARD; PRT; 14 AA.  
 ID ADFA\_TENMO  
 AC P82965;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Antidiuretic factor A (ADFA) (ADF) (Antidiuretic hormone A) (ADHA).  
 OS Tenebrio molitor (Yellow mealworm).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
 CC Tenebrionidae; Tenebrio.  
 OX NCBI\_TaxID=7067;  
 RN [1]  
 RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.  
 RC TISSUE=Head;  
 RX MEDLINE=21642653; PubMed=11756661;  
 RA Eigenheer R.A., Nicolson S.W., Schegg K.M., Hull J.J., Schooley D.A.;  
 RT "Identification of a potent antidiuretic factor acting on beetle  
 Malpighian tubules.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:84-89(2002).  
 CC -1- FUNCTION: Strong inhibitor of fluid secretion by the Malpighian



CC tubules. Uses cGMP as a second messenger and inhibits fluid  
 CC production by decreasing cAMP concentration.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- MASS SPECTROMETRY: MW=1541.58; METHOD=MALDI.  
 CC -1- SIMILARITY: STRONG, TO THE C-TERMINAL OF T.MOLLITOR CUTICULAR  
 CC PROTEIN LPCP29.  
 DR GO:0005576; C:extracellular; NAS.  
 DR GO:0005184; F:neuropeptide hormone activity; NAS.  
 DR GO:0007218; P:neuropeptide signaling pathway; NAS.  
 KM Neuropeptide; Hormone.  
 SQ SEQUENCE 14 AA; 1543 MW; F49C91A3F16E43D1 CRC64;

Query Match 23.3%; Score 14; DB 1; Length 14;  
 Best Local Similarity 42.9%; Pred. No. 9.2e+03;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 NSKFRV 10  
 | : | |  
 Db 3 NTPGHAV 9

Search completed: August 30, 2004, 10:50:20  
 Job time : 1.89527 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 3.30743 Seconds  
(without alignments)  
319.918 Million cell updates/sec

Title: US-09-720-469A-4  
Perfect score: 60  
Sequence: 1 GYKNSKFRHVI 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID     | Description        |
|------------|-------|-------------|--------|----|--------|--------------------|
| 1          | 25    | 41.7        | 14     | 2  | PT0254 | Ig heavy chain CRD |
| 2          | 23    | 38.3        | 13     | 2  | PT0331 | Ig heavy chain CRD |
| 3          | 22    | 36.7        | 12     | 2  | PH1454 | T-cell receptor al |
| 4          | 22    | 36.7        | 12     | 2  | PC4377 | telomeric and tetr |
| 5          | 22    | 36.7        | 13     | 2  | PH0787 | T-cell receptor al |
| 6          | 21    | 35.0        | 10     | 2  | B61033 | ranatachykinin B - |
| 7          | 20    | 33.3        | 9      | 2  | JP0073 | ribosomal protein  |
| 8          | 20    | 33.3        | 11     | 2  | PT0211 | T-cell receptor al |
| 9          | 20    | 33.3        | 14     | 2  | S22236 | lipoxigenase (EC 1 |
| 10         | 20    | 33.3        | 14     | 2  | S29486 | GTP-binding protei |
| 11         | 19    | 31.7        | 8      | 2  | S65381 | cytochrome-c oxida |
| 12         | 19    | 31.7        | 13     | 2  | A61361 | bradykinin-like pe |
| 13         | 19    | 31.7        | 13     | 2  | S47356 | T-cell antigen rec |
| 14         | 18    | 30.0        | 8      | 2  | JS0316 | leucokinin VI - Ma |
| 15         | 18    | 30.0        | 12     | 2  | PT0274 | Ig heavy chain CRD |
| 16         | 18    | 30.0        | 13     | 2  | AS9387 | VCAM-1 5'UTR bindi |
| 17         | 17    | 28.3        | 9      | 2  | D58503 | translation elonga |
| 18         | 17    | 28.3        | 10     | 2  | S65387 | cytochrome-c oxida |
| 19         | 17    | 28.3        | 10     | 2  | PC4374 | telomeric and tetr |
| 20         | 17    | 28.3        | 11     | 2  | IS4193 | Rhesus blood group |
| 21         | 17    | 28.3        | 11     | 2  | PH0939 | T-cell receptor be |
| 22         | 17    | 28.3        | 14     | 2  | S36678 | dodecenoyl-CoA Del |
| 23         | 16    | 26.7        | 9      | 2  | D57444 | neuropeptide Grb-A |
| 24         | 16    | 26.7        | 9      | 2  | A42266 | peptidylglycine mo |
| 25         | 16    | 26.7        | 10     | 1  | ECLQ4M | tachykinin IV - mi |
| 26         | 16    | 26.7        | 10     | 2  | PT0243 | Ig heavy chain CRD |
| 27         | 16    | 26.7        | 11     | 2  | S23373 | T-cell receptor al |
| 28         | 16    | 26.7        | 12     | 2  | S01222 | translation elonga |
| 29         | 16    | 26.7        | 12     | 2  | S10624 | lipovitelin - Afr  |

|    |    |      |    |   |        |                    |
|----|----|------|----|---|--------|--------------------|
| 30 | 16 | 26.7 | 13 | 2 | A44818 | extracellular lipa |
| 31 | 16 | 26.7 | 13 | 2 | S63492 | dissimilatory sulf |
| 32 | 16 | 26.7 | 13 | 2 | E60396 | antigen 7H8/2 - ma |
| 33 | 16 | 26.7 | 13 | 2 | PS0443 | potassium channel  |
| 34 | 16 | 26.7 | 14 | 2 | A01250 | angiotensin precur |
| 35 | 16 | 26.7 | 14 | 2 | PT0252 | Ig heavy chain CRD |
| 36 | 16 | 26.7 | 14 | 2 | PC0709 | unidentified 27.2K |
| 37 | 15 | 25.0 | 8  | 2 | S37141 | rpsA protein - Erw |
| 38 | 15 | 25.0 | 8  | 2 | B27867 | homeotic protein U |
| 39 | 15 | 25.0 | 9  | 2 | PT0324 | Ig heavy chain CRD |
| 40 | 15 | 25.0 | 9  | 2 | S78420 | ribosomal protein  |
| 41 | 15 | 25.0 | 10 | 2 | A24867 | scyllorhizin I - s |
| 42 | 15 | 25.0 | 11 | 2 | PC2372 | 58K heat shock pro |
| 43 | 15 | 25.0 | 11 | 2 | S23926 | major glycoprotein |
| 44 | 15 | 25.0 | 12 | 2 | C30503 | Ig gamma-2b chain  |
| 45 | 15 | 25.0 | 13 | 2 | S32471 | lymadFamide 1 - g  |

## ALIGNMENTS

RESULT 1  
PT0254  
Ig heavy chain CRD3 region (clone 2-115A) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0254  
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A/Reference number: PT0222; MUID:91108337; PMID:1899102  
A/Accession: PT0254  
A/Molecule type: DNA  
A/Residues: 1-14 <YAM>  
A/Experimental source: B lymphocyte  
A/Keywords: heterotetramer; immunoglobulin

Query Match 41.7%; Score 25; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKNSKFRH 9  
DB 7 YDSSGYHR 14

## RESULT 2

PT0331  
Ig heavy chain CRD3 region (clone J2-121) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0331  
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A/Reference number: PT0222; MUID:91108337; PMID:1899102  
A/Accession: PT0331  
A/Molecule type: DNA  
A/Residues: 1-13 <YAM>  
A/Experimental source: B lymphocyte  
A/Keywords: heterotetramer; immunoglobulin

Query Match 38.3%; Score 23; DB 2; Length 13;  
Best Local Similarity 57.1%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKNSKF 7  
DB 6 GYNNPPF 12

## RESULT 3

PH1454

T-cell receptor alpha chain (clone A3/72.2) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
C:Accession: PH1454  
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Parnetier, C.; Regnault, A.; Kc  
J. Exp. Med. 177, 811-820, 1993  
A:Title: T cell receptor selection by and recognition of two class I major histocompatib  
A:Reference number: PH1430; MUID:93171821; PMID:8436911  
A:Accession: PH1454  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>  
A:Experimental source: cytolytic T-lymphocyte  
C:Superfamily: immunoglobulin homology  
C:Keywords: receptor; T-cell

Query Match 36.7%; Score 22; DB 2; Length 12;  
Best Local Similarity 57.1%; Pred. No. 5.7e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKNSKF 7  
||:|  
Db 5 GYQNFYF 11

## RESULT 4

PC4377  
telomeric and tetraplex DNA binding protein qTBP42 VIII - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Oct-1997 #sequence\_revision 28-Oct-1997 #text\_change 07-May-1999  
C:Accession: PC4377  
R:Sarig, G.; Weisman-Shomer, P.; Fry, M.  
Biochem. Biophys. Res. Commun. 237, 617-623, 1997  
A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA  
A:Reference number: PC4371; MUID:97445086; PMID:9299414  
A:Accession: PC4377  
A:Molecule type: protein  
A:Residues: 1-12 <SAR>  
C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 36.7%; Score 22; DB 2; Length 12;  
Best Local Similarity 80.0%; Pred. No. 5.7e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 KEHHRV 10  
|||  
Db 3 KEHTV 7

## RESULT 5

PH0787  
T-cell receptor alpha chain (F8) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PH0787  
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-r  
allelic exclusion and antigen-specific repertoire.  
A:Reference number: PH0746; MUID:92078846; PMID:1836010  
A:Accession: PH0787  
A:Molecule type: mRNA  
A:Residues: 1-13 <CAS>  
A:Cross-references: EMBL:X60891  
A:Experimental source: T lymphocyte  
C:Keywords: T-cell receptor

Query Match 36.7%; Score 22; DB 2; Length 13;  
Best Local Similarity 57.1%; Pred. No. 6.2e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYKNSKF 7  
||:|  
Db 6 GYQNFYF 12

## RESULT 6

B61033

ranatachykinin B - bullfrog  
C:Species: Rana catesbeiana (bullfrog)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Aug-2000  
C:Accession: B61033; JE0427  
R:Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.  
Regul. Pept. 42(Suppl.1), S12, 1992  
A:Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intest  
A:Reference number: A61033  
A:Accession: B61033  
A:Molecule type: protein  
A:Residues: 1-10 <KAN>  
R:Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.  
Biochem. Biophys. Res. Commun. 177, 588-595, 1991  
A:Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intest  
A:Reference number: JE0426; MUID:91254337; PMID:2043143  
A:Accession: JE0427  
A:Molecule type: protein  
A:Residues: 1-10 <KOZ>  
C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end; neuropeptide  
F:10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 35.0%; Score 21; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 7.3e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKNSKFF 8  
||:|  
Db 1 YKSDSFY 7

## RESULT 7

JP0073

ribosomal protein L32 - Leuconostoc mesenteroides (fragment)  
C:Species: Leuconostoc mesenteroides  
C:Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 28-Oct-1994  
C:Accession: JP0073  
R:Ochi, K.  
submitted to JIPID, February 1994  
A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pro  
A:Reference number: JP0042  
A:Accession: JP0073  
A:Molecule type: protein  
A:Residues: 1-9 <OCH>  
C:Keywords: protein biosynthesis; ribosome

Query Match 33.3%; Score 20; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNSK 6  
|||  
Db 6 KNSK 9

## RESULT 8

PT0211

T-cell receptor alpha chain V-J region (4-1-G.4) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997  
C:Accession: PT0211  
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.  
J. Exp. Med. 173, 1091-1097, 1991  
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict  
A:Reference number: PT0209; MUID:91217621; PMID:1902501  
A:Accession: PT0211  
A:Molecule type: mRNA  
A:Residues: 1-11 <NAK>  
C:Keywords: T-cell receptor

Query Match 33.3%; Score 20; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYKN 4  
|:|  
8 GYQN 11

## RESULT 9

S22236  
lipoxigenase (EC 1.13.11.12) 1 - barley (fragment)  
C/Species: Hordeum vulgare (barley)  
C/Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999  
C/Accession: S22236  
R/Doderer, A.; Kokkelink, I.; van der Veen, S.; Valk, B.E.; Schram, A.W.; Douma, A.C.  
Biochim. Biophys. Acta 1120, 97-104, 1992  
A/Title: Purification and characterization of two lipoxigenase isoenzymes from germinati  
A/Reference number: S21772; MUID:92207997; PMID:1554746  
A/Accession: S22236  
A/Molecule type: protein  
A/Residues: 1-14 <DOD>  
A/Experimental source: var. Triumph, seed  
C/Function:  
A/Description: catalyzes the peroxidation of polyunsaturates fatty acids to their corres  
C/Superfamily: lipoxigenase  
C/Keywords: monomer; oxidoreductase; seed

Query Match 33.3%; Score 20; DB 2; Length 14;  
Best Local Similarity 37.5%; Pred. No. 1.6e+03;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKNSKFR 9  
|:|:|  
7 YPNTSDHK 14

## RESULT 10

S29486  
GTP-binding protein o-rab3 - electric ray (Discofyge ommata) (fragment)  
C/Species: Discofyge ommata  
C/Date: 22-Nov-1993 #sequence\_revision 27-Feb-1997 #text\_change 13-Mar-1997  
C/Accession: S29486  
R/Volkhardt, W.; Pevsner, J.; Elferink, L.A.; Scheller, R.H.  
FEBS Lett. 317, 53-56, 1993  
A/Title: Association of three small GTP-binding proteins with cholinergic synaptic vesic  
A/Reference number: S29485; MUID:93154521; PMID:8428634  
A/Accession: S29486  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-14 <VOL>

Query Match 33.3%; Score 20; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 NSKFRV 11  
|:|:|  
6 NQNFNAVI 13

## RESULT 11

S65381  
cytochrome-c oxidase (EC 1.9.3.1) chain VIIb, hepatic - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
C/Accession: S65381  
R/Schaegeer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.  
Eur. J. Biochem. 230, 235-241, 1995  
A/Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term  
A/Reference number: S65372; MUID:95324529; PMID:7601105  
A/Accession: S65381

A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-8 <SCH>  
C/Keywords: oxidoreductase

Query Match 31.7%; Score 19; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FHR 9  
|:|  
6 FHR 8

## RESULT 12

A61361  
bradykinin-like peptide - Bombina orientalis  
C/Species: Bombina orientalis  
C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 18-Aug-2000  
C/Accession: A61361  
R/Yasuhara, T.; Hira, M.; Nakajima, T.; Yanaihara, N.; Yanaihara, C.; Hashimoto, T.; Saki  
Chem. Pharm. Bull. 21, 1388-1391, 1973  
A/Title: Active peptides on smooth muscle in the skin of Bombina orientalis Boulenger an  
A/Reference number: A61361; MUID:73256822; PMID:4732297  
A/Accession: A61361  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-13 <YAS>  
C/Superfamily: unassigned animal peptides  
C/Keywords: skin

Query Match 31.7%; Score 19; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KFH 8  
|:|  
11 KFH 13

## RESULT 13

S47358  
T-cell antigen receptor VJ junction beta chain - human  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
C/Accession: S47358  
R/lehner, P.J.  
submitted to the EMBL Data Library, August 1994  
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c  
A/Reference number: S47355  
A/Accession: S47358  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-13 <LEH>  
A/Cross-references: EMBL:Z35682; NID:G527453; PIDN:CAA84751.1; PID:G527454  
C/Keywords: T-cell receptor

Query Match 31.7%; Score 19; DB 2; Length 13;  
Best Local Similarity 42.9%; Pred. No. 2.3e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKNSKFR 8  
|:|:|  
6 YRNQPOH 12

## RESULT 14

JS0316  
leucokinin VI - Madeira cockroach  
C/Species: Leucophaea maderae (Madeira cockroach)  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
C/Accession: JS0316  
R/Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 27-30, 1987  
A:Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic  
A:Reference number: JS0315  
A:Accession: JS0316  
A:Molecule type: protein  
A:Residues: 1-8 <HOL>  
C:Comment: Leucokinins, a family of cephalomycotropic peptides, stimulate contractile act  
C:Keywords: amidated carboxyl end; cephalomycotropic peptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 30.0%; Score 18; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SKFH 8  
|||  
Db 2 SSFH 5

RESULT 15  
PT0274  
Ig heavy chain CRD3 region (clone 3-109B) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0274  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0274  
A:Molecule type: DNA  
A:Residues: 1-12 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 18; DB 2; Length 12;  
Best Local Similarity 60.0%; Pred. No. 3.3e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKS 5  
|||  
Db 2 GYSS 6

RESULT 16  
A59387  
VCAM-1 5'UTR binding protein - Rana pipiens (fragment)  
C:Species: Rana pipiens  
C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
C:Accession: A59387  
R:BANERJEE, H.  
submitted to the Protein Sequence Database, February 2001  
A:Description: Identification and characterization of a novel VCAM-1 5'UTR.  
A:Reference number: A59387  
A:Accession: A59387  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <BAN>  
A:Experimental source: CCL-145  
A>Note: VCAM-1 5' untranslated region binding protein with a probable translation inhibi

Query Match 30.0%; Score 18; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYK 3  
|||  
Db 8 GYK 10

RESULT 17  
D58503

translation elongation factor EF-Tu - unidentified bacterium (fragment)  
C:Species: unidentified bacterium  
C:Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 28-May-1999  
C:Accession: D58503  
R:Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A:Description: The proteins of kidney and gallbladder stones.  
A:Reference number: A58501  
A:Accession: D58503  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <BIN>  
A:Experimental source: human bile and stones  
C:Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog

Query Match 28.3%; Score 17; DB 2; Length 9;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYKSKFHR 9  
|||:  
Db 1 GYRPFYFR 9

RESULT 18  
S65387  
cytochrome-c oxidase (EC 1.9.3.1) chain VII b, cardiac - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 16-Jul-1999  
C:Accession: S65387; S65386  
R:Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.  
Eur. J. Biochem. 230, 235-241, 1995  
A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term  
A:Reference number: S65372; MUID:95324529; PMID:7601105  
A:Accession: S65387  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <SCH>  
A:Accession: S65386  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <SC2>  
C:Keywords: cardiac muscle; heart; oxidoreductase

Query Match 28.3%; Score 17; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4.3e+03;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSKPFH 8  
|||  
Db 5 KPTPFH 10

RESULT 19  
PC4374  
telomeric and tetraplex DNA binding protein qTBP42 IV - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Oct-1997 #sequence\_revision 28-Oct-1997 #text\_change 07-May-1999  
C:Accession: PC4374  
R:Sarig, G.; Weisman-Shomer, P.; Fry, M.  
Biochem. Biophys. Res. Commun. 237, 617-623, 1997  
A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA  
A:Reference number: PC4371; MUID:97445086; PMID:9299414  
A:Accession: PC4374  
A:Molecule type: protein  
A:Residues: 1-10 <SAR>  
C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 28.3%; Score 17; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 4.3e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 NSKEHRV 10  
: |||:  
Db 4 DXKEHRL 10

## RESULT 20

Rhesus blood group CcEe protein - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 21-Jul-2000  
C/Accession: I54193  
R/Cherif-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartron, J.P.; Colin, Y.  
Genomics 19, 68-74, 1994  
A/Title: Organization of the gene (RHCE) encoding the human blood group RhCCE antigens  
A/Reference number: I54193; MUID:94245182; PMID:8188244  
A/Accession: I54193  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-11 <RES>  
A/Cross-references: GB:S70456; NID:9546795; PIDN:AAD14061.1; PID:94261761  
C/Genetics:  
A/Gene: GDB:RHCE  
A/Cross-references: GDB:229957; OMIM:111700  
A/Map position: 1p36.2-1p34

Query Match 28.3%; Score 17; DB 2; Length 11;  
Best Local Similarity 37.5%; Pred. No. 4.7e+03;  
Matches 3; Conservative 2; Indels 0; Gaps 0;

QY 4 NSKEHRV 11  
: |||:  
Db 2 SSKYPRSV 9

## RESULT 21

T-cell receptor beta chain V-D-J region (clone 10) - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C/Accession: PH0939  
R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A/Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy  
A/Reference number: PH0891; MUID:92078857; PMID:1836012  
A/Accession: PH0939  
A/Molecule type: mRNA  
A/Residues: 1-11 <GOL>  
A/Experimental source: complete Freund's adjuvant-immunized lymph node  
C/Keywords: T-cell receptor

Query Match 28.3%; Score 17; DB 2; Length 11;  
Best Local Similarity 60.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKNS 5  
: |||:  
Db 7 GLKNT 11

## RESULT 22

dodecenoyl-CoA Delta-isomerase (EC 5.3.3.8) / enoyl-CoA hydratase (EC 4.2.1.17) / 3-hydr  
S36678  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Mar-1997 #sequence\_revision 07-Nov-1997 #text\_change 24-Jul-1998  
C/Accession: S36678  
R/Chen, N.; Crane, D.I.  
Biochem. J. 283, 605-610, 1992  
A/Title: Induction of the major integral membrane protein of mouse liver peroxisomes by  
A/Reference number: S21285; MUID:92246895; PMID:1575703  
A/Accession: S36678  
A/Molecule type: protein  
A/Residues: 1-14 <CHE>  
A/Experimental source: liver

C/Function:  
A/Pathway: fatty acid beta-oxidation  
C/Keywords: carbon-oxygen lyase; fatty acid beta-oxidation; hydro-lyase; intramolecular

Query Match 28.3%; Score 17; DB 2; Length 14;  
Best Local Similarity 42.9%; Pred. No. 6.1e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKSKF 7  
: |||:  
Db 2 GFKMGPF 8

## RESULT 23

neuropeptide Grb-ASR B4 - two-spotted cricket  
D57444  
C/Species: Gryllus bimaculatus (two-spotted cricket)  
C/Date: 26-Jan-1996 #sequence\_revision 26-Jan-1996 #text\_change 26-Jan-1996  
C/Accession: D57444  
R/Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.  
J. Biol. Chem. 270, 21103-21108, 1995  
A/Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cri  
A/Reference number: A57444; MUID:95403341; PMID:7673141  
A/Accession: D57444  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-9 <LOR>

Query Match 26.7%; Score 16; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 KFH 8  
: |||:  
Db 4 RFH 6

## RESULT 24

peptidylglycine monooxygenase (EC 1.14.17.3), rPAM-5 - rat (fragment)  
A42266  
N/Alternate names: peptidylglycine alpha-amidating monooxygenase  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 26-May-1995  
C/Accession: A42266  
R/Eipper, B.A.; Green, C.B.; Campbell, T.A.; Stoffers, D.A.; Keutmann, H.T.; Mains, R.E.  
J. Biol. Chem. 267, 4008-4015, 1992  
A/Title: Alternative splicing and endoproteolytic processing generate tissue-specific fo  
A/Reference number: A42266; MUID:92156145; PMID:1740449  
A/Accession: A42266  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-9 <EIP>  
A/Experimental source: pituitary  
A/Note: sequence extracted from NCBI backbone (NCBIN:82733, NCBIPI:82750)  
C/Keywords: oxidoreductase

Query Match 26.7%; Score 16; DB 2; Length 9;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYKNS 5  
: |||:  
Db 4 GFKDT 8

## RESULT 25

ECLQ4M  
tachykinin IV - migratory locust  
N/Alternate names: locusttachykinin IV  
C/Species: Locusta migratoria (migratory locust)  
C/Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 08-Dec-1995  
C/Accession: B60073  
R/Schoofs, L.; Holman, G.M.; Hayes, T.K.; Kochansky, J.P.; Nachman, R.J.; De Loof, A.

Regul. Pept. 31, 199-212, 1990  
A;Title: Locusttachykinin IIR and IV: two additional insect neuropeptides with homology  
A;Reference number: A60073; MUID:91219696; PMID:2132575  
A;Accession: B60073  
A;Molecule type: Protein  
A;Residues: 1-10 <SCH>  
C;Superfamily: tachykinin  
C;Keywords: amidated carboxyl end; neuropeptide: tachykinin  
F;10/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 26.7%; Score 16; DB 1; Length 10;  
Best Local Similarity 75.0%; Pred. No. 6.6e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FHRV 10  
| | |  
Db 6 FHGV 9

## RESULT 26

PT0243  
IG heavy chain CRD3 region (clone 2-103A) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0243  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0243  
A;Molecule type: DNA  
A;Residues: 1-10 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 26.7%; Score 16; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 6.6e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKS 5  
| | |  
Db 2 GYDS 6

## RESULT 27

S23373  
T-cell receptor alpha chain J region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C;Accession: S23373  
R;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichman  
Eur. J. Immunol. 21, 2749-2754, 1991  
A;Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheu  
A;Reference number: S23364; MUID:92037820; PMID:1657615  
A;Accession: S23373  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-11 <PLU>  
A;Cross-references: EMBL:X58168  
C;Keywords: T-cell receptor

Query Match 26.7%; Score 16; DB 2; Length 11;  
Best Local Similarity 42.9%; Pred. No. 7.3e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SKFHRV 11  
| | |  
Db 4 SNYDKV 10

## RESULT 28

S01222  
translation elongation factor EF-Tu - Pseudomonas aeruginosa (fragment)

C;Species: Pseudomonas aeruginosa  
C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 26-Aug-1999  
C;Accession: S01222  
R;Hughes, M.A.; Jones, D.S.  
Nucleic Acids Res. 16, 7193, 1988  
A;Title: A fragment of the Pseudomonas aeruginosa genome contains five tRNA genes, four  
A;Reference number: S01222; MUID:88303352; PMID:3136442  
A;Accession: S01222  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-12 <HUG>  
A;Cross-references: EMBL:X07950; NID:G45426; PIDN:CAA30775.1; PID:G45427  
C;Genetics: tuFB  
A;Gene: tuFB  
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog  
C;Keywords: GTP binding; protein biosynthesis

Query Match 26.7%; Score 16; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 8e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 KFHR 9  
| | |  
Db 5 KFER 8

## RESULT 29

S10624  
lipovitelin - African clawed frog  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995  
C;Accession: S10624  
R;Wallace, R.A.; Hoch, K.L.; Carnevali, O.  
J. Mol. Biol. 213, 407-409, 1990  
A;Title: Placement of small lipovitelin subunits within the vitellogenin precursor in Xe  
A;Reference number: S10624; MUID:90278951; PMID:2352275  
A;Accession: S10624  
A;Molecule type: protein  
A;Residues: 1-12 <WAL>

Query Match 26.7%; Score 16; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 8e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 KFHR 9  
| | |  
Db 1 KFOR 4

## RESULT 30

A44818  
extracellular lipase - Pseudomonas aeruginosa (fragment)  
C;Species: Pseudomonas aeruginosa  
C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 31-Oct-1997  
C;Accession: A44818  
R;Gilbert, E.J.; Cornish, A.; Jones, C.W.  
J. Gen. Microbiol. 137, 2223-2229, 1991  
A;Title: Purification and properties of extracellular lipase from Pseudomonas aeruginosa  
A;Reference number: A44818; MUID:92085040; PMID:1748875  
A;Accession: A44818  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-13 <GIL>  
A;Experimental source: strain TE3285  
A;Note: sequence extracted from NCBI backbone (NCBIP:70395)  
C;Superfamily: Pseudomonas triacylglycerol lipase

Query Match 26.7%; Score 16; DB 2; Length 13;  
Best Local Similarity 30.0%; Pred. No. 8.7e+03;  
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 YKSKFHRV 11  
| | |



Db 3 YPQTKYPIVL 12

## RESULT 31

S63492  
dissimilatory sulfite reductase beta chain, soluble - Desulfovibrio desulfuricans (fragm  
C/Species: Desulfovibrio desulfuricans  
C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
C/Accession: S63492  
R/Steuwer, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.  
Eur. J. Biochem. 233, 873-879, 1995  
A/Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio  
A/Reference number: S63489; MUID:96085152; PMID:8521853  
A/Accession: S63492  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-13 <STE>

Query Match 26.7%; Score 16; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 8.7e+03;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKNSK 6  
|||  
Db 6 GYNPKK 11

## RESULT 32

E60396  
antigen 7H8/2 - malaria parasite (Plasmodium falciparum) (fragments)  
C/Species: Plasmodium falciparum  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jun-2000  
C/Accession: E60396  
R/Limpaiboon, T.; Taylor, D.W.; Jones, G.; Geysen, H.M.; Saul, A.  
Southeast Asian J. Trop. Med. Public Health 21, 388-396, 1990  
A/Title: Characterization of a Plasmodium falciparum epitope recognized by a monoclonal  
A/Reference number: A60396; MUID:91164876; PMID:1706114  
A/Accession: E60396  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-13 <LIM>  
A/Cross-references: GB:M31305

Query Match 26.7%; Score 16; DB 2; Length 13;  
Best Local Similarity 33.3%; Pred. No. 8.7e+03;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKNSKFHRV 10  
:|:|:|  
Db 1 FLKSEFMKV 9

## RESULT 33

PS0443  
potassium channel protein S10 G3 - fruit fly (Drosophila melanogaster) (fragment)  
C/Species: Drosophila melanogaster  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Feb-1997  
C/Accession: PS0443  
R/Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bond  
Neuron 9, 209-216, 1992  
A/Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.  
A/Reference number: JH0697; MUID:92360298; PMID:1497890  
A/Accession: PS0443  
A/Status: nucleic acid sequence not shown  
A/Molecule type: mRNA  
A/Residues: 1-13 <ADE>  
C/Comment: This potassium channel is activated by calcium.  
C/Genetics:  
A/Gene: FlyBase:s10  
A/Cross-references: FlyBase:FBgn0003429  
C/Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

Query Match 26.7%; Score 16; DB 2; Length 13;

Best Local Similarity 42.9%; Pred. No. 8.7e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SKFHRVI 11  
|||  
Db 7 SKFDDIV 13

## RESULT 34

A01250  
angiotensin precursor - horse (fragment)  
C/Species: Equus caballus (domestic horse)  
C/Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 15-Sep-2003  
C/Accession: A92775; A01250  
R/Skeggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.  
J. Exp. Med. 106, 439-453, 1957  
A/Reference number: A92775  
A/Accession: A92775  
A/Molecule type: protein  
A/Residues: 1-14 <SKE>  
C/Superfamily: Serpin  
C/Keywords: blood pressure control; hormone; vasoconstrictor  
F/1-10/Product: angiotensin I #status experimental <AN1>  
F/1-8/Product: angiotensin II #status experimental <AN2>

Query Match 26.7%; Score 16; DB 2; Length 14;  
Best Local Similarity 40.0%; Pred. No. 9.4e+03;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 FHRVI 11  
|||  
Db 8 FHLIV 12

## RESULT 35

PT0252  
Ig heavy chain CRD3 region (clone 2-109D) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0252  
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A/Reference number: PT0222; MUID:91108337; PMID:1899102  
A/Accession: PT0252  
A/Molecule type: DNA  
A/Residues: 1-14 <YAM>  
A/Experimental source: B lymphocyte  
C/Keywords: heterotetramer; immunoglobulin

Query Match 26.7%; Score 16; DB 2; Length 14;  
Best Local Similarity 33.3%; Pred. No. 9.4e+03;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKNSKFHRV 10  
:|:|:|  
Db 6 YDSSGYVYV 14

## RESULT 36

PC7079  
unidentified 27.2K protein - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C/Accession: PC7079  
R/Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;  
Electrophoresis 21, 1853-1871, 2000  
A/Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of t  
A/Reference number: PC7072  
A/Accession: PC7079  
A/Molecule type: protein  
A/Residues: 1-14 <TSU>  
A/Experimental source: strain C57BL/6Cr Slc, male; brain, striatum

C;Keywords: brain

Query Match 26.7%; Score 16; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 9.4e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 YKNSK 6  
|||  
Db 4 YVNKK 8

## RESULT 37

S37141

IPSA protein - Erwinia chrysanthemi

C;Species: Erwinia chrysanthemi

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Oct-1999

C;Accession: S37141

R;Douille, A.; Tousseint, A.; Faelen, M.

submitted to the EMBL Data Library, August 1993

A;Description: Identification of the integration host factor genes of E. chrysanthemi.

A;Reference number: S37139

A;Accession: S37141

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-8 &lt;DOU&gt;

A;Cross-references: EMBL:X74750; NID:g399669; PIDD:CAA52769.1; PID:g581108

Query Match 25.0%; Score 15; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 YKNSK 6  
|||  
Db 2 FKSAX 6

## RESULT 38

B27867

homeotic protein Ultrabithorax - fruit fly (Drosophila melanogaster) (fragment)

C;Species: Drosophila melanogaster

C;Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 23-Feb-1997

C;Accession: B27867

R;Saari, G.; Bienz, M.

EMBO J. 6, 1775-1779, 1987

A;Title: The structure of the ultrabithorax promoter of Drosophila melanogaster.

A;Reference number: A91072

A;Accession: B27867

A;Molecule type: mRNA

A;Residues: 1-8 &lt;SAA&gt;

C;Genetics:

A;Gene: FlyBase:Ubx

A;Cross-references: FlyBase:Fggn0003944

C;Keywords: DNA binding; nucleus; transcription regulation

Query Match 25.0%; Score 15; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 NSKFR 9  
|||  
Db 2 NSYFEQ 7

## RESULT 39

PT0324

Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0324

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0324  
A;Molecule type: DNA  
A;Residues: 1-9 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotrimer; immunoglobulin

Query Match 25.0%; Score 15; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GYKNS 5  
|||  
Db 3 GYGES 7

## RESULT 40

S78420

ribosomal protein RL41, mitochondrial [validated] - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jul-2000

C;Accession: S78420

R;Goldschmidt-Reisin, S.; Graack, H.R.

submitted to the Protein Sequence Database, February 1998

A;Reference number: S78411

A;Accession: S78420

A;Molecule type: protein

A;Residues: 1-9 &lt;GOL&gt;

A;Note: the protein is designated as mitochondrial ribosomal protein L41  
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 25.0%; Score 15; DB 2; Length 9;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 SKFHRV 10  
|||  
Db 2 NOXHRL 7

## RESULT 41

A24867

scyllorhinn I - smaller spotted catshark

C;Species: Scyllorhinn canicula (smaller spotted catshark, smaller spotted dogfish)

C;Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 18-Aug-2000

C;Accession: A24867; S33301

R;Conlon, J.M.; Deacon, C.F.; O'Toole, L.; Thim, L.

FEBS Lett. 200, 111-116, 1986

A;Title: Scyllorhinn I and II: two novel tachykinins from dogfish gut.

A;Reference number: A91359; MUID:86192829; PMID:2422058

A;Accession: A24867

A;Molecule type: protein

A;Residues: 1-10 &lt;CON&gt;

A;Cross-references: 1-10 &lt;CON&gt;

R;Wang, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.

Eur. J. Biochem. 214, 469-474, 1993

A;Title: Primary structures and biological activities of substance-P-related peptides from

A;Reference number: S33300; MUID:93292508; PMID:7685693

A;Accession: S33301

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 &lt;WAO&gt;

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; neuropeptide

F;10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 25.0%; Score 15; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 KNSKFR 8  
|||  
Db 2 KFDKFX 7

## RESULT 42

PC2372  
58K heat shock protein groEL [similarity] - Bacillus cereus (strain ts-4) (fragment)  
C/Species: Bacillus cereus  
C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C/Accession: PC2372  
R/Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.  
Biosci. Biotechnol. Biochem. 59, 231-235, 1995  
A/Title: Identification of DNA-binding proteins changed after induction of sporulation  
A/Reference number: PC2369; MUID:95218265; PMID:7766022  
A/Accession: PC2372  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-11 <MAS>  
C/Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 25.0%; Score 15; DB 2; Length 11;  
Best Local Similarity 60.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSKF 7  
|: ||  
Db 2 KDIF 6

## RESULT 43

S23926  
major glycoprotein PAS-6 - bovine (fragment)  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 19-Mar-1997 #sequence\_revision 01-Feb-1999 #text\_change 01-Feb-1999  
C/Accession: S23926  
R/Kim, D.H.; Kanno, C.; Mizokami, Y.  
Biochim. Biophys. Acta 1122, 203-211, 1992  
A/Title: Purification and characterization of major glycoproteins, PAS-6 and PAS-7, from  
A/Reference number: S23926; MUID:92353107; PMID:1643094  
A/Accession: S23926  
A/Molecule type: protein  
A/Residues: 1-11 <KIM>  
C/Keywords: glycoprotein; milk; blocked amino end

Query Match 25.0%; Score 15; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKN 4  
|||  
Db 3 GNKN 6

## RESULT 44

C30503  
Ig gamma-2b chain C region (F5.5.1) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 16-Aug-1996  
C/Accession: C30503  
R/Gilmore, G.L.; Bard, J.A.; Birshstein, B.K.  
J. Immunol. 141, 1754-1761, 1988  
A/Title: DNA rearrangements affecting both variable and constant regions of Ig H chain  
A/Reference number: A30503; MUID:88315788; PMID:2842402  
A/Accession: C30503  
A/Molecule type: mRNA  
A/Residues: 1-12 <GIL>  
A/Experimental source: myeloma cell line  
C/Keywords: immunoglobulin

Query Match 25.0%; Score 15; DB 2; Length 12;  
Best Local Similarity 42.9%; Pred. No. 1.2e+04;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSKFHR 9  
: |||  
Db 1 ENYNGHR 7

## RESULT 45

S32471  
LymnadFamide 1 - great pond snail  
C/Species: Lymnaea stagnalis (great pond snail)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999  
C/Accession: S32471  
R/Johnsen, A.H.; Rehfeld, J.F.  
Eur. J. Biochem. 213, 875-879, 1993  
A/Title: LymnadFamides, a new family of neuropeptides from the pond snail, Lymnaea stagn  
A/Reference number: S32471; MUID:93238777; PMID:8477756  
A/Accession: S32471  
A/Molecule type: protein  
A/Residues: 1-13 <JOH>  
A/Cross-references: PIDN:AAB26362.1; PID:G299829  
A/Experimental source: ganglia  
C/Keywords: amidated carboxyl end; neuropeptide  
F.13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 25.0%; Score 15; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 1.3e+04;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSKF 7  
|||  
Db 7 NSAF 10

Search completed: August 30, 2004, 10:58:49  
Job time : 4.30743 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 13.4527 Seconds  
(without alignments)  
257.253 Million cell updates/sec

Title: US-09-720-469A-4  
Perfect score: 60  
Sequence: 1 GYKSKFHRVI 11

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 149443

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description                         |
|------------|-------|-------------|--------|----|-------------------------------------|
| 1          | 32    | 53.3        | 9      | 16 | US-10-447-161-84 Sequence 84, Appl  |
| 2          | 32    | 53.3        | 9      | 16 | US-10-788-016-1 Sequence 1, Appl1   |
| 3          | 27    | 45.0        | 11     | 14 | US-10-105-232-266 Sequence 266, App |
| 4          | 27    | 45.0        | 11     | 14 | US-10-189-437-253 Sequence 253, App |
| 5          | 26.5  | 44.2        | 12     | 9  | US-09-226-666-1 Sequence 1, Appl1   |
| 6          | 26.5  | 44.2        | 12     | 9  | US-09-226-666-13 Sequence 13, Appl  |
| 7          | 26.5  | 44.2        | 12     | 9  | US-09-226-666-16 Sequence 16, Appl  |
| 8          | 26    | 43.3        | 8      | 12 | US-10-462-452-459 Sequence 459, App |
| 9          | 26    | 43.3        | 8      | 16 | US-10-601-953-588 Sequence 588, App |
| 10         | 26    | 43.3        | 8      | 16 | US-10-322-266-460 Sequence 460, App |
| 11         | 26    | 43.3        | 9      | 9  | US-09-780-053-158 Sequence 158, App |
| 12         | 26    | 43.3        | 9      | 15 | US-10-380-705-12 Sequence 12, Appl  |
| 13         | 26    | 43.3        | 10     | 9  | US-09-780-053-180 Sequence 180, App |
| 14         | 26    | 43.3        | 10     | 9  | US-09-780-053-304 Sequence 304, App |
| 15         | 26    | 43.3        | 10     | 9  | US-09-780-053-399 Sequence 399, App |

|    |    |      |    |    |                    |                   |
|----|----|------|----|----|--------------------|-------------------|
| 16 | 26 | 43.3 | 10 | 10 | US-09-572-270A-759 | Sequence 759, App |
| 17 | 26 | 43.3 | 10 | 12 | US-10-462-452-413  | Sequence 413, App |
| 18 | 26 | 43.3 | 10 | 16 | US-10-601-953-541  | Sequence 541, App |
| 19 | 26 | 43.3 | 10 | 16 | US-10-322-266-414  | Sequence 414, App |
| 20 | 26 | 43.3 | 14 | 14 | US-10-239-313A-642 | Sequence 642, App |
| 21 | 25 | 41.7 | 8  | 13 | US-10-014-485A-116 | Sequence 116, App |
| 22 | 25 | 41.7 | 11 | 12 | US-10-289-456-91   | Sequence 91, Appl |
| 23 | 25 | 41.7 | 12 | 9  | US-09-982-172-186  | Sequence 186, App |
| 24 | 25 | 41.7 | 12 | 9  | US-09-982-172-245  | Sequence 245, App |
| 25 | 25 | 41.7 | 13 | 14 | US-10-174-105A-153 | Sequence 153, App |
| 26 | 25 | 41.7 | 14 | 12 | US-10-289-456-108  | Sequence 108, App |
| 27 | 25 | 41.7 | 14 | 14 | US-10-105-232-267  | Sequence 267, App |
| 28 | 25 | 41.7 | 14 | 14 | US-10-105-232-270  | Sequence 270, App |
| 29 | 25 | 41.7 | 14 | 14 | US-10-189-437-254  | Sequence 254, App |
| 30 | 25 | 41.7 | 14 | 14 | US-10-189-437-257  | Sequence 257, App |
| 31 | 24 | 40.0 | 8  | 9  | US-09-910-552-16   | Sequence 16, Appl |
| 32 | 24 | 40.0 | 8  | 16 | US-10-643-465-16   | Sequence 16, Appl |
| 33 | 24 | 40.0 | 9  | 15 | US-10-117-937-555  | Sequence 555, App |
| 34 | 24 | 40.0 | 10 | 9  | US-09-780-053-472  | Sequence 472, App |
| 35 | 24 | 40.0 | 10 | 9  | US-09-753-126-126  | Sequence 126, App |
| 36 | 24 | 40.0 | 10 | 10 | US-09-896-896A-90  | Sequence 90, Appl |
| 37 | 24 | 40.0 | 10 | 14 | US-10-319-340-8    | Sequence 8, Appl  |
| 38 | 24 | 40.0 | 10 | 15 | US-10-117-937-556  | Sequence 556, App |
| 39 | 24 | 40.0 | 10 | 15 | US-10-330-697-126  | Sequence 126, App |
| 40 | 24 | 40.0 | 11 | 10 | US-09-791-393-21   | Sequence 21, Appl |
| 41 | 24 | 40.0 | 11 | 10 | US-09-791-389-21   | Sequence 21, Appl |
| 42 | 24 | 40.0 | 11 | 16 | US-10-264-309-22   | Sequence 22, Appl |
| 43 | 24 | 40.0 | 12 | 12 | US-10-302-100B-12  | Sequence 12, Appl |
| 44 | 24 | 40.0 | 14 | 9  | US-09-734-002-5    | Sequence 5, Appl1 |
| 45 | 24 | 40.0 | 14 | 10 | US-09-932-613-39   | Sequence 39, Appl |

ALIGNMENTS

RESULT 1  
US-10-447-161-84  
; Sequence 84, Application US/10447161  
; Publication No. US20040023314A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Rong-fu  
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis  
; FILE REFERENCE: HO-P02484US1  
; CURRENT APPLICATION NUMBER: US/10/447,161  
; CURRENT FILING DATE: 2003-05-28  
; PRIOR APPLICATION NUMBER: 60/383,530  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 84  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-10-447-161-84

Query Match 53.3%; Score 32; DB 16; Length 9;  
Best Local Similarity 100.0%; Pred. NO. 1.2e+06;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KFHRI 11  
Db 1 KFHRI 6

RESULT 2  
US-10-788-016-1  
; Sequence 1, Application US/10788016  
; Publication No. US2004014192A1  
; GENERAL INFORMATION:  
; APPLICANT: ITOH, Kyogo  
; TITLE OF INVENTION: Desensitizers

```
; FILE REFERENCE: 3190-049
; CURRENT APPLICATION NUMBER: US/10/788,016
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/JP02/08641
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: JP P2001-260046
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 84th residue
; OTHER INFORMATION: to the 92nd residue of cyclophilin B
US-10-788-016-1
```

```
Query Match          53.3%; Score 32; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 KFHRYV 11
      |||||
Db      1 KFHRYV 6
```

```
RESULT 3
US-10-105-232-266
; Sequence 266, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCCH, SAMUEL
; APPLICANT: BOGOCCH, ELENORE S.
; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: Patentin 2.1
; SEQ ID NO 266
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Influenza virus
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: gly or gln
US-10-105-232-266
```

```
Query Match          45.0%; Score 27; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4 NSKFRV 10
      |||||
Db      3 NEKFHXI 9
```

```
RESULT 4
US-10-189-437-253
; Sequence 253, Application US/10189437
```

```
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCCH, SAMUEL
; APPLICANT: BOGOCCH, ELENORE S.
; TITLE OF INVENTION: REPLICIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: Patentin 2.1
; SEQ ID NO 253
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Influenza virus
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: gly or gln
US-10-189-437-253
```

```
Query Match          45.0%; Score 27; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4 NSKFRV 10
      |||||
Db      3 NEKFHXI 9
```

```
RESULT 5
US-09-226-666-1
; Sequence 1, Application US/09226666A
; Patent No. US20020077282A1
; GENERAL INFORMATION:
; APPLICANT: Spaccapoli, Peter
; APPLICANT: Rothstein, David M.
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
; FILE REFERENCE: 50032/007001
; CURRENT APPLICATION NUMBER: US/09/226,666A
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Internal fragment
US-09-226-666-1
```

```
Query Match          44.2%; Score 26.5; DB 9; Length 12;
Best Local Similarity 75.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      1 GYKSKFH 8
      |||||
Db      6 GYKR-KFH 12
```

```
RESULT 6
US-09-226-666-13
; Sequence 13, Application US/09226666A
; Patent No. US20020077282A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Spacciapoli, Peter
; APPLICANT: Rothenstein, David M.
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
; FILE REFERENCE: 50032/007001
; CURRENT APPLICATION NUMBER: US/09/226,666A
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from Homo sapiens
US-09-226-666-13
```

```
Query Match      44.2%; Score 26.5; DB 9; Length 12;
Best Local Similarity 75.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      1 GYKNSKFH 8
      ||| |||
Db      6 GYK-QKFH 12
```

```
RESULT 7
US-09-226-666-16
; Sequence 16, Application US/09226666A
; Patent No. US20020077282A1
; GENERAL INFORMATION:
; APPLICANT: Spacciapoli, Peter
; APPLICANT: Rothenstein, David M.
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
; FILE REFERENCE: 50032/007001
; CURRENT APPLICATION NUMBER: US/09/226,666A
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from Homo sapiens
US-09-226-666-16
```

```
Query Match      44.2%; Score 26.5; DB 9; Length 12;
Best Local Similarity 75.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      1 GYKNSKFH 8
      ||| |||
Db      6 GYK-KKFH 12
```

```
RESULT 8
US-10-462-452-459
; Sequence 459, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
```

```
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 459
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-459
```

```
Query Match      43.3%; Score 26; DB 12; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 KNSKPFH 8
      :|||
Db      1 RNSSFH 6
```

```
RESULT 9
US-10-601-953-588
; Sequence 588, Application US/10601953
; Publication No. US20040077540A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; FILE REFERENCE: 02-03US
; CURRENT APPLICATION NUMBER: US/10/601,953
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 588
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-588
```

```
Query Match      43.3%; Score 26; DB 16; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 KNSKPFH 8
      :|||
Db      1 RNSSFH 6
```

```
RESULT 10
US-10-322-266-460
; Sequence 460, Application US/10322266
; Publication No. US20040115135A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptide
; TITLE OF INVENTION: YY And Methods For Treating And Preventing Obesity
; FILE REFERENCE: NPC10567
; CURRENT APPLICATION NUMBER: US/10/322,266
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 797
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 460
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-322-266-460
```

```
Query Match      43.3%; Score 26; DB 16; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
```

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSKRF 8  
:|:|:|  
Db 1 RNSSEF 6

## RESULT 11

US-09-780-053-158  
; Sequence 158, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 158  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-158

Query Match 43.3%; Score 26; DB 9; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKSKRF 8  
|:|:|:|:  
Db 1 GHONSTFY 8

## RESULT 12

US-10-380-705-12  
; Sequence 12, Application US/10380705  
; Publication No. US20040019919A1  
; GENERAL INFORMATION:  
; APPLICANT: Universit,t Zurich  
; TITLE OF INVENTION: Calcium binding proteins  
; FILE REFERENCE: Calsyntenins  
; CURRENT APPLICATION NUMBER: US/10/380,705  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: EP 00810830.0  
; PRIOR FILING DATE: 2000-09-14  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-10-380-705-12

Query Match 43.3%; Score 26; DB 15; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKNSKRF 8  
|:|:|:|:  
Db 2 YKPAERF 8

## RESULT 13

US-09-780-053-180  
; Sequence 180, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 180  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-180

Query Match 43.3%; Score 26; DB 9; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4.9e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKSKRF 8  
|:|:|:|:  
Db 2 GHONSTFY 9

## RESULT 14

US-09-780-053-304  
; Sequence 304, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 304  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-304

Query Match 43.3%; Score 26; DB 9; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4.9e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKSKRF 8  
|:|:|:|:  
Db 1 GHONSTFY 8

## RESULT 15

US-09-780-053-399



```
; Sequence 399, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Chailita-Bid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappel1 Mitchell
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.SUSU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 399
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-399

Query Match          43.3%; Score 26; DB 9; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYKNSKPH 8
Db 1 GHQNSTFY 8

RESULT 16
US-09-572-270A-759
; Sequence 759, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 759
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in GL2. at 99-108 and may interact with
US-09-572-270A-759

Query Match          43.3%; Score 26; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSKPHR 9
Db 1 KRKYTHR 7

RESULT 17
US-10-462-452-413
; Sequence 413, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
```

```
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 413
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-413

Query Match          43.3%; Score 26; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSKPH 8
Db 1 RNSSFH 6

RESULT 18
US-10-601-953-541
; Sequence 541, Application US/10601953
; Publication No. US20040077540A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; FILE REFERENCE: 02-03US
; CURRENT APPLICATION NUMBER: US/10/601,953
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 541
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-541

Query Match          43.3%; Score 26; DB 16; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSKPH 8
Db 1 RNSSFH 6

RESULT 19
US-10-322-266-414
; Sequence 414, Application US/10322266
; Publication No. US20040115135A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptide
; TITLE OF INVENTION: YY And Methods For Treating And Preventing Obesity
; FILE REFERENCE: NPC10567
; CURRENT APPLICATION NUMBER: US/10/322,266
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 797
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 414
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Synthetic construct  
US-10-322-266-414

Query Match  
Best Local Similarity 43.3%; Score 26; DB 16; Length 10;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KNSKFH 8  
Db 1 RNSSFH 6

RESULT 20

US-10-239-313A-642  
; Sequence 642, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGER - HAMOUR, Christine  
; APPLICANT: CORVALA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: Patentn Ver. 2.1  
; SEQ ID NO 642  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Clostridium tetani  
US-10-239-313A-642

Query Match  
Best Local Similarity 43.3%; Score 26; DB 14; Length 14;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KNSKF 7  
Db 5 KNSKF 9

RESULT 21

US-10-014-485A-116  
; Sequence 116, Application US/10014485A  
; Publication No. US20020168684A1  
; GENERAL INFORMATION:  
; APPLICANT: Cell Signaling Technology, Inc.  
; APPLICANT: COMB, Michael J.  
; APPLICANT: ZHANG, Hui  
; APPLICANT: TAN, Yi  
; TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIES U  
; TITLE OF INVENTION: PEPTIDE LIBRARIES AS ANTIGENS  
; FILE REFERENCE: CST-138 CIP2  
; CURRENT APPLICATION NUMBER: US/10/014,485A  
; CURRENT FILING DATE: 2002-03-18  
; PRIOR APPLICATION NUMBER: US 09/148,712  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: US 09/535,364  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 145  
; SOFTWARE: Patentn version 3.1  
; SEQ ID NO 116  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

NAME/KEY: MOD\_RES  
; LOCATION: (5)-(5)  
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 5 is phosphorylated  
US-10-014-485A-116

Query Match  
Best Local Similarity 41.7%; Score 25; DB 13; Length 8;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GYKSKFH 8  
Db 1 GWKNSIRH 8

RESULT 22

US-10-289-456-91  
; Sequence 91, Application US/10289456  
; Publication No. US20040033211A1  
; GENERAL INFORMATION:  
; APPLICANT: Bachmann, Martin  
; APPLICANT: Maurer, Patrick  
; APPLICANT: Spohn, Gunther  
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease  
; FILE REFERENCE: 1700.0330001  
; CURRENT APPLICATION NUMBER: US/10/289,456  
; CURRENT FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: PCT/IB02/00166  
; PRIOR FILING DATE: 2002-01-21  
; PRIOR APPLICATION NUMBER: US 10/050,902  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/396,635  
; PRIOR FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: US 60/331,045  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: Patentn version 3.2  
; SEQ ID NO 91  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: RANKL peptide EF loop  
US-10-289-456-91

Query Match  
Best Local Similarity 41.7%; Score 25; DB 12; Length 11;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 NSKFH 8  
Db 6 NSEFH 10

RESULT 23

US-09-982-172-186  
; Sequence 186, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: Patentn version 3.1  
; SEQ ID NO 186  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide

US-09-982-172-186

Query Match 41.7%; Score 25; DB 9; Length 12;  
Best Local Similarity 50.0%; Pred. No. 8.9e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKNSKFHR 9  
| : | : | :  
Db 5 YVNSSFYK 12

## RESULT 24

US-09-982-172-245  
; Sequence 245, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THERAGAINS, AND METHODS, SYSTEMS AND KITS FOR GENERAT  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 245  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-245

Query Match 41.7%; Score 25; DB 9; Length 12;  
Best Local Similarity 50.0%; Pred. No. 8.9e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKNSKFHR 9  
| : | : | :  
Db 5 YVNSSFYK 12

## RESULT 25

US-10-174-105A-153  
; Sequence 153, Application US/10174105A  
; Publication No. US20030068652A1  
; GENERAL INFORMATION:  
; APPLICANT: Cell Signaling Technology, Inc.  
; APPLICANT: ZHANG, Hui  
; APPLICANT: COMB, Michael J.  
; APPLICANT: TAN, Yi  
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,  
; TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING  
; FILE REFERENCE: CST-138 CIP3  
; CURRENT APPLICATION NUMBER: US/10/174,105A  
; CURRENT FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: US 09/148,712  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: US 09/535,364  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 193  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 153  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: (8)..(8)  
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 8 is phosphorylated  
US-10-174-105A-153

Query Match 41.7%; Score 25; DB 14; Length 13;  
Best Local Similarity 62.5%; Pred. No. 9.6e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYNSKFH 8  
| : | : | :  
Db 4 GWKNSIRH 11

## RESULT 26

US-10-289-456-108  
; Sequence 108, Application US/10289456  
; Publication No. US20040033211A1  
; GENERAL INFORMATION:  
; APPLICANT: Bachmann, Martin  
; APPLICANT: Maurer, Patrick  
; APPLICANT: Spohn, Gunther  
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease  
; FILE REFERENCE: 1700.0330001  
; CURRENT APPLICATION NUMBER: US/10/289,456  
; CURRENT FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: PCT/IB02/00166  
; PRIOR FILING DATE: 2002-01-21  
; PRIOR APPLICATION NUMBER: US 10/050,902  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/396,635  
; PRIOR FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: US 60/331,045  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 108  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: RANKL peptide EF loop  
US-10-289-456-108

Query Match 41.7%; Score 25; DB 12; Length 14;  
Best Local Similarity 80.0%; Pred. No. 1e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NSKFH 8  
| : | : | :  
Db 9 NSEFH 13

## RESULT 27

US-10-105-232-267  
; Sequence 267, Application US/10105232  
; Publication No. US20030180328A1  
; GENERAL INFORMATION:  
; APPLICANT: BOGACH, SAMUEL  
; APPLICANT: BOGACH, ELENORE S.  
; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS  
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS  
; FILE REFERENCE: 09425-46904  
; CURRENT APPLICATION NUMBER: US/10/105,232  
; CURRENT FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: 60/303,396  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/278,761  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: 09/146,755  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: 09/817,144  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: 08/198,139  
; PRIOR FILING DATE: 1994-02-17  
; NUMBER OF SEQ ID NOS: 535  
; SOFTWARE: PatentIn 2.1

; SEQ ID NO 267  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Influenza virus  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)  
; OTHER INFORMATION: val or leu  
US-10-105-232-267

Query Match 41.7%; Score 25; DB 14; Length 14;  
Best Local Similarity 80.0%; Pred. No. 1e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSKPH 8  
|  
|  
|  
Db 10 NEKPH 14

RESULT 28  
US-10-105-232-270  
; Sequence 270, Application US/10105232  
; Publication No. US20030180328A1  
; GENERAL INFORMATION:  
; APPLICANT: BOGGOCH, SAMUEL  
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS  
; FILE REFERENCE: 09425-46904  
; CURRENT APPLICATION NUMBER: US/10/105,232  
; CURRENT FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: 60/303,396  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/278,761  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: 09/146,755  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: 09/817,144  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: 08/198,139  
; PRIOR FILING DATE: 1994-02-17  
; NUMBER OF SEQ ID NOS: 535  
; SOFTWARE: PatentIn 2.1  
; SEQ ID NO 270  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Influenza virus  
US-10-105-232-270

Query Match 41.7%; Score 25; DB 14; Length 14;  
Best Local Similarity 80.0%; Pred. No. 1e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSKPH 8  
|  
|  
|  
Db 10 NEKPH 14

RESULT 29  
US-10-189-437-254  
; Sequence 254, Application US/10189437  
; Publication No. US20030194414A1  
; GENERAL INFORMATION:  
; APPLICANT: BOGGOCH, SAMUEL  
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE  
; FILE REFERENCE: 09425/46905  
; CURRENT APPLICATION NUMBER: US/10/189,437  
; CURRENT FILING DATE: 2002-07-08  
; PRIOR APPLICATION NUMBER: 10/105,232  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: 09/984,057  
; PRIOR FILING DATE: 2001-10-26

; PRIOR APPLICATION NUMBER: 60/303,396  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/278,761  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 729  
; SOFTWARE: PatentIn 2.1  
; SEQ ID NO 254  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Influenza virus  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)  
; OTHER INFORMATION: val or leu  
US-10-189-437-254

Query Match 41.7%; Score 25; DB 14; Length 14;  
Best Local Similarity 80.0%; Pred. No. 1e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSKPH 8  
|  
|  
|  
Db 10 NEKPH 14

RESULT 30  
US-10-189-437-257  
; Sequence 257, Application US/10189437  
; Publication No. US20030194414A1  
; GENERAL INFORMATION:  
; APPLICANT: BOGGOCH, SAMUEL  
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE  
; FILE REFERENCE: 09425/46905  
; CURRENT APPLICATION NUMBER: US/10/189,437  
; CURRENT FILING DATE: 2002-07-08  
; PRIOR APPLICATION NUMBER: 10/105,232  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: 09/984,057  
; PRIOR FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: 60/303,396  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/278,761  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 729  
; SOFTWARE: PatentIn 2.1  
; SEQ ID NO 257  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Influenza virus  
US-10-189-437-257

Query Match 41.7%; Score 25; DB 14; Length 14;  
Best Local Similarity 80.0%; Pred. No. 1e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSKPH 8  
|  
|  
|  
Db 10 NEKPH 14

RESULT 31  
US-09-910-552-16  
; Sequence 16, Application US/09910552  
; Publication No. US20020197260A1  
; GENERAL INFORMATION:  
; APPLICANT: Granoff, Dan M.  
; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE  
; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE  
; FILE REFERENCE: 1238.002  
; CURRENT APPLICATION NUMBER: US/09/910,552

```
/ CURRENT FILING DATE: 2001-07-23
/ PRIOR APPLICATION NUMBER: 09/494,822
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 68
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 16
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: sequence from
US-09-910-552-16
```

```
Query Match          40.0%; Score 24; DB 9; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 GYKNSKFH 8
      ||: ||
Db      1 GYEVQPFH 8
```

```
RESULT 32
US-10-643-465-16
/ Sequence 16, Application US/10643465
/ Publication No. US20040077840A1
/ GENERAL INFORMATION:
/ APPLICANT: Granoff, Dan M.
/ APPLICANT: Moe, Gregory R.
/ TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
/ TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
/ FILE REFERENCE: 1238.002
/ CURRENT APPLICATION NUMBER: US/10/643,465
/ CURRENT FILING DATE: 2003-08-19
/ PRIOR APPLICATION NUMBER: US/08/925,002
/ PRIOR FILING DATE: 1997-08-27
/ NUMBER OF SEQ ID NOS: 68
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 16
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: sequence from
/ OTHER INFORMATION: a phage display peptide library
US-10-643-465-16
```

```
Query Match          40.0%; Score 24; DB 16; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 GYKNSKFH 8
      ||: ||
Db      1 GYEVQPFH 8
```

```
RESULT 33
US-10-117-937-555
/ Sequence 555, Application US/10117937
/ Publication No. US20030220239A1
/ GENERAL INFORMATION:
/ APPLICANT: CTL IMMUNO THERAPIES CORP.
/ APPLICANT: SIMARD, John, J.L.
/ APPLICANT: DIAMOND, David, C.
/ APPLICANT: LIU, Liping
/ APPLICANT: XIE, Zhidong
/ TITLE OF INVENTION: EPITOPE SEQUENCES
/ FILE REFERENCE: CTLLM.027A
/ CURRENT APPLICATION NUMBER: US/10/117,937
/ CURRENT FILING DATE: 2002-04-04
/ PRIOR APPLICATION NUMBER: US 60/282,211
```

```
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: US 60/337,017
/ PRIOR FILING DATE: 2001-11-07
/ PRIOR APPLICATION NUMBER: US 60/363,210
/ PRIOR FILING DATE: 2002-03-07
/ NUMBER OF SEQ ID NOS: 602
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 555
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-117-937-555
```

```
Query Match          40.0%; Score 24; DB 15; Length 9;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 YKNSKFHRV 10
      ||: ||
Db      1 YDNKQFEKI 9
```

```
RESULT 34
US-09-780-053-472
/ Sequence 472, Application US/09780053
/ Patent No. US20020102640A1
/ GENERAL INFORMATION:
/ APPLICANT: Rene S. Hubert
/ APPLICANT: Daniel E.H. Afar
/ APPLICANT: Pia M. Challita-Bid
/ APPLICANT: Mary Paris
/ APPLICANT: Elana Levin
/ APPLICANT: Steve Chappell Mitchell
/ TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
/ TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
/ FILE REFERENCE: 129.5USU1
/ CURRENT APPLICATION NUMBER: US/09/780,053
/ CURRENT FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/181,261
/ PRIOR FILING DATE: 2000-02-09
/ NUMBER OF SEQ ID NOS: 716
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 472
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-780-053-472
```

```
Query Match          40.0%; Score 24; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 GYKNSKF 7
      ||: ||
Db      4 GHQNSTF 10
```

```
RESULT 35
US-09-753-126-126
/ Sequence 126, Application US/09753126
/ Patent No. US20020127219A1
/ GENERAL INFORMATION:
/ APPLICANT: OKKELS, JENS SIGURD
/ APPLICANT: JENSEN, ANNE DAM
/ APPLICANT: HALKIER, TORBEN
/ APPLICANT: JENSEN, RIKKE BOLDING
/ TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME
/ FILE REFERENCE: 31-000600US
/ CURRENT APPLICATION NUMBER: US/09/753,126
/ CURRENT FILING DATE: 2001-06-11
/ PRIOR APPLICATION NUMBER: PA 1999 01891
```

PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: 60/174,652  
PRIOR FILING DATE: 2000-01-06  
PRIOR APPLICATION NUMBER: PA 200 00865  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: 60/210,984  
PRIOR FILING DATE: 2000-06-12  
PRIOR APPLICATION NUMBER: 60/211,124  
PRIOR FILING DATE: 2000-06-12  
PRIOR APPLICATION NUMBER: PA 2000 01027  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: 60/217,497  
PRIOR FILING DATE: 2000-07-11  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 126  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-753-126-126

Query Match 40.0%; Score 24; DB 9; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1.1e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKNSKFFH 8  
|||:|:  
Db 4 YKSYKFFY 10

RESULT 36  
US-09-896-896A-90  
Sequence 90, Application US/09896896A  
Publication No. US20030036181A1  
GENERAL INFORMATION:  
APPLICANT: MAXYGEN APS  
TITLE OF INVENTION: PEPTIDE EXTENDED GLYCOSYLATED POLYPEPTIDES  
FILE REFERENCE: 0217US210  
CURRENT APPLICATION NUMBER: US/09/896,896A  
CURRENT FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: US 60/217,497  
PRIOR FILING DATE: 2000-07-11  
PRIOR APPLICATION NUMBER: US 60/225,558  
PRIOR FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: DK PA 2000 01027  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DK PA 2000 01092  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: PCT/DK00/00743  
PRIOR FILING DATE: 2000-12-29  
PRIOR APPLICATION NUMBER: PCT/DK01/00090  
PRIOR FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 90  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-896-896A-90

Query Match 40.0%; Score 24; DB 10; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1.1e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKNSKFFH 8  
|||:|:  
Db 4 YKSYKFFY 10

RESULT 37  
US-10-319-340-8  
Sequence 8, Application US/10319340  
Publication No. US20030144211A1  
GENERAL INFORMATION:  
APPLICANT: Heavner, George A.  
APPLICANT: McEvey, Rodger P.  
APPLICANT: Geng, Jian-Guo  
TITLE OF INVENTION: Peptide Inhibitors of Inflammation Mediated by Selectins  
FILE REFERENCE: CTC 102 CON DIV  
CURRENT APPLICATION NUMBER: US/10/319,340  
CURRENT FILING DATE: 2002-12-13  
PRIOR APPLICATION NUMBER: 08/135,319  
PRIOR FILING DATE: 1993-10-12  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 8  
LENGTH: 10  
TYPE: PRT  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic inhibitory peptide  
US-10-319-340-8

Query Match 40.0%; Score 24; DB 14; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKNSK 6  
|||:|:  
Db 1 YKNNK 5

RESULT 38  
US-10-117-937-556  
Sequence 556, Application US/10117937  
Publication No. US20030220239A1  
GENERAL INFORMATION:  
APPLICANT: CTL IMMUNO THERAPIES CORP.  
APPLICANT: SIMARD, John, J.L.  
APPLICANT: DIAMOND, David, C.  
APPLICANT: LIU, Liping  
APPLICANT: XIE, Zhidong  
TITLE OF INVENTION: EPITOPE SEQUENCES  
FILE REFERENCE: CTLIMM.027A  
CURRENT APPLICATION NUMBER: US/10/117,937  
CURRENT FILING DATE: 2002-04-04  
PRIOR APPLICATION NUMBER: US 60/282,211  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: US 60/337,017  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: US 60/363,210  
PRIOR FILING DATE: 2002-03-07  
NUMBER OF SEQ ID NOS: 602  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 556  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-117-937-556

Query Match 40.0%; Score 24; DB 15; Length 10;  
Best Local Similarity 33.3%; Pred. No. 1.1e+03;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKNSKPHRV 10  
|||:|:  
Db 2 YDNKQPEKI 10

RESULT 39

US-10-330-697-126  
; Sequence 126, Application US/10330697  
; Publication No. US20040009165A1  
; GENERAL INFORMATION:  
; APPLICANT: OKKELS, JENS SIGURD  
; APPLICANT: JENSEN, ANNE DAM  
; APPLICANT: HALKIER, TORBEN  
; APPLICANT: JENSEN, RIKKE BOLDING  
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME  
; TITLE OF INVENTION: ACTIVATORS  
; FILE REFERENCE: 31-000600US  
; CURRENT APPLICATION NUMBER: US/10/330,697  
; CURRENT FILING DATE: 2002-12-27  
; PRIOR APPLICATION NUMBER: US/09/753,126  
; PRIOR FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: PA 1999 01891  
; PRIOR FILING DATE: 1999-12-30  
; PRIOR APPLICATION NUMBER: 60/174,652  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: PA 200 00865  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 60/210,984  
; PRIOR FILING DATE: 2000-06-12  
; PRIOR APPLICATION NUMBER: 60/211,124  
; PRIOR FILING DATE: 2000-06-12  
; PRIOR APPLICATION NUMBER: PA 2000 01027  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/217,497  
; PRIOR FILING DATE: 2000-07-11  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 126  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-330-697-126

Query Match 40.0%; Score 24; DB 15; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1.1e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKNSKFEH 8  
||: ||:  
Db 4 YKSYKFEY 10

RESULT 40  
US-09-791-393-21  
; Sequence 21, Application US/09791393  
; Publication No. US20030032200A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri  
; APPLICANT: Parekh, Rajesh Bhikhu  
; APPLICANT: Rohlf, Christian  
; TITLE OF INVENTION: Proteins, Genes and Their Use for  
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)  
; TITLE OF INVENTION: and Unipolar Depression  
; FILE REFERENCE: 2543-1-001 N1  
; CURRENT APPLICATION NUMBER: US/09/791,393  
; CURRENT FILING DATE: 2002-01-02  
; EARLIER APPLICATION NUMBER: GB 0004412.3  
; EARLIER FILING DATE: 2000-02-24  
; EARLIER APPLICATION NUMBER: GB 0030050.9  
; EARLIER FILING DATE: 2000-12-08  
; EARLIER APPLICATION NUMBER: US 60/254,830  
; EARLIER FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 11

TYPE: PRT  
; ORGANISM: homo sapien  
US-09-791-393-21

Query Match 40.0%; Score 24; DB 10; Length 11;  
Best Local Similarity 44.4%; Pred. No. 1.2e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKNSKFEH 9  
||: ||:  
Db 3 GYLNTGYQR 11

RESULT 41  
US-09-791-389-21  
; Sequence 21, Application US/09791389  
; Publication No. US20030032773A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri  
; APPLICANT: Parekh, Rajesh Bhikhu  
; APPLICANT: Rohlf, Christian  
; APPLICANT: Terrect, Jonathan Alexander  
; APPLICANT: Tyson, Kerry Louise  
; TITLE OF INVENTION: Proteins, Genes and Their Use for  
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)  
; TITLE OF INVENTION: and Unipolar Depression  
; FILE REFERENCE: 2543-1-001 N2  
; CURRENT APPLICATION NUMBER: US/09/791,389  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: GB 0004412.3  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: GB 0030050.9  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: US 60/254,830  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-09-791-389-21

Query Match 40.0%; Score 24; DB 10; Length 11;  
Best Local Similarity 44.4%; Pred. No. 1.2e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKNSKFEH 9  
||: ||:  
Db 3 GYLNTGYQR 11

RESULT 42  
US-10-264-309-22  
; Sequence 22, Application US/10264309  
; Publication No. US20040022794A1  
; GENERAL INFORMATION:  
; APPLICANT: DURHAM, L. KATHRYN  
; APPLICANT: FRIEDMAN, DAVID L.  
; APPLICANT: HERATH, HERATH  
; APPLICANT: KIMMEL, LIDA H.  
; APPLICANT: PAREKH, RAJESH B.  
; APPLICANT: POTTER, DAVID M.  
; APPLICANT: ROHLFF, CHRISTIAN  
; APPLICANT: SILBER, B. MICHAEL  
; APPLICANT: SNYDER, PETER J.  
; APPLICANT: SOARES, HOLLY D.  
; APPLICANT: STIGER, THOMAS R.  
; APPLICANT: SUNDERLAND, P. TREY  
; APPLICANT: TOWNSEND, ROBERT R.  
; APPLICANT: WHITE, W. FROST  
; APPLICANT: WILLIAMS, STEPHEN A.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,

;; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE  
;; FILE REFERENCE: FOA-002.01  
;; CURRENT APPLICATION NUMBER: US/10/264,309  
;; CURRENT FILING DATE: 2002-10-03  
;; PRIOR APPLICATION NUMBER: 60/326,708  
;; PRIOR FILING DATE: 2001-10-03  
;; NUMBER OF SEQ ID NOS: 491  
;; SOFTWARE: Patentin Version 2.1  
;; SEQ ID NO 22  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-264-309-22

Query Match 40.0%; Score 24; DB 16; Length 11;  
Best Local Similarity 44.4%; Pred. No. 1.2e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKSKFHR 9  
|||:|  
Db 3 GYLTGTGYQR 11

RESULT 43  
US-10-302-100B-12  
;; Sequence 12, Application US/10302100B  
;; Publication No. US20040054131A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ballinger, Marcus  
;; TITLE OF INVENTION: Synthetic Peptides Having FGF Receptor  
;; FILE REFERENCE: 035784/263218  
;; CURRENT APPLICATION NUMBER: US/10/302,100B  
;; CURRENT FILING DATE: 2002-11-21  
;; PRIOR APPLICATION NUMBER: 09/407,687  
;; PRIOR FILING DATE: 1999-09-28  
;; PRIOR APPLICATION NUMBER: 60/102,667  
;; PRIOR FILING DATE: 1998-09-30  
;; NUMBER OF SEQ ID NOS: 43  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 12  
;; LENGTH: 12  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: synthetic peptide  
US-10-302-100B-12

Query Match 40.0%; Score 24; DB 12; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKSKFHR 8  
|||:|  
Db 5 GYYSCTFH 12

RESULT 44  
US-09-734-002-5  
;; Sequence 5, Application US/09734002  
;; Patent No. US20010016333A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Motoharu SEIKI et al.  
;; TITLE OF INVENTION: NOVEL PROTEIN AND MONOCLONAL ANTIBODY SPECIFIC THERETO  
;; NUMBER OF SEQUENCES: 14  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
;; STREET: 2033 K Street, N.W., Suite 800  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: U.S.A.  
;; ZIP: 20006

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: MS-DOS  
;; SOFTWARE: Wordperfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/734,002  
;; FILING DATE: 12-Dec-2000  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/JP96/01956  
;; FILING DATE: July 12, 1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Lee Cheng  
;; REGISTRATION NUMBER: 40,949  
;; REFERENCE/DOCKET NUMBER: <Unknown>  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-721-8200  
;; TELEFAX: 202-721-8250  
;; TELEX: <Unknown>  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14  
;; TYPE: Amino acid  
;; STRANDEDNESS: Single  
;; TOPOLOGY: Linear  
;; MOLECULE TYPE: Peptide  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-734-002-5

Query Match 40.0%; Score 24; DB 9; Length 14;  
Best Local Similarity 80.0%; Pred. No. 1.6e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NSKFEH 8  
:||||  
Db 5 SSKFEH 9

RESULT 45  
US-09-932-613-39  
;; Sequence 39, Application US/09932613  
;; Publication No. US20030091565A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Human Genome Sciences, Inc.  
;; APPLICANT: Belzer, James P.  
;; APPLICANT: Potter, M. Daniel  
;; APPLICANT: Fleming, Tony J.  
;; APPLICANT: Rosen, Craig A.  
;; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
;; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
;; CURRENT APPLICATION NUMBER: US/09/932,613  
;; CURRENT FILING DATE: 2001-08-17  
;; NUMBER OF SEQ ID NOS: 458  
;; SOFTWARE: Patentin version 3.1  
;; SEQ ID NO 39  
;; LENGTH: 14  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-39

Query Match 40.0%; Score 24; DB 10; Length 14;  
Best Local Similarity 66.7%; Pred. No. 1.6e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSKFEH 8  
|||:|  
Db 9 KHCKFEH 14

Search completed: August 30, 2004, 11:04:56



Thu Sep 2 07:41:37 2004

us-09-720-469a-4.aug30.rapb

Page 13

Job time : 14.4527 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 4.34797 Seconds  
(without alignments)  
130.609 Million cell updates/sec

Title: US-09-720-469A-4  
Perfect score: 60  
Sequence: 1 GYKNSKFRVY 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID                | Description       |
|------------|-------|-------------|--------|----|-------------------|-------------------|
| 1          | 26.5  | 44.2        | 11     | 1  | US-08-481-888A-19 | Sequence 19, Appl |
| 2          | 26.5  | 44.2        | 11     | 1  | US-08-485-273A-19 | Sequence 19, Appl |
| 3          | 26.5  | 44.2        | 11     | 2  | US-08-973-563A-19 | Sequence 19, Appl |
| 4          | 26.5  | 44.2        | 11     | 2  | US-08-973-559-19  | Sequence 19, Appl |
| 5          | 26.5  | 44.2        | 12     | 1  | US-08-481-888A-18 | Sequence 18, Appl |
| 6          | 26.5  | 44.2        | 12     | 1  | US-08-485-273A-18 | Sequence 18, Appl |
| 7          | 26.5  | 44.2        | 12     | 2  | US-08-973-563A-18 | Sequence 18, Appl |
| 8          | 26.5  | 44.2        | 12     | 2  | US-08-973-563A-24 | Sequence 25, Appl |
| 9          | 26.5  | 44.2        | 12     | 2  | US-08-973-563A-25 | Sequence 25, Appl |
| 10         | 26.5  | 44.2        | 12     | 2  | US-08-973-563A-27 | Sequence 27, Appl |
| 11         | 26.5  | 44.2        | 12     | 2  | US-08-973-563A-36 | Sequence 36, Appl |
| 12         | 26.5  | 44.2        | 12     | 2  | US-08-973-559-18  | Sequence 24, Appl |
| 13         | 26.5  | 44.2        | 12     | 2  | US-08-973-559-24  | Sequence 25, Appl |
| 14         | 26.5  | 44.2        | 12     | 2  | US-08-973-559-25  | Sequence 27, Appl |
| 15         | 26.5  | 44.2        | 12     | 2  | US-08-973-559-27  | Sequence 27, Appl |
| 16         | 26.5  | 44.2        | 12     | 2  | US-08-973-559-36  | Sequence 36, Appl |
| 17         | 26.5  | 44.2        | 12     | 3  | US-08-993-235-4   | Sequence 4, Appl  |
| 18         | 26.5  | 44.2        | 12     | 3  | US-08-993-235-5   | Sequence 5, Appl  |
| 19         | 26.5  | 44.2        | 12     | 3  | US-08-993-235-7   | Sequence 7, Appl  |
| 20         | 26.5  | 44.2        | 12     | 4  | US-09-226-666-1   | Sequence 1, Appl  |
| 21         | 26.5  | 44.2        | 12     | 4  | US-09-226-666-13  | Sequence 13, Appl |
| 22         | 26.5  | 44.2        | 12     | 4  | US-09-226-666-16  | Sequence 16, Appl |
| 23         | 26.5  | 44.2        | 12     | 4  | US-08-993-235-4   | Sequence 4, Appl  |
| 24         | 26.5  | 44.2        | 12     | 4  | US-08-993-235-5   | Sequence 5, Appl  |
| 25         | 26.5  | 44.2        | 12     | 4  | US-08-993-235-7   | Sequence 7, Appl  |
| 26         | 26.5  | 44.2        | 14     | 1  | US-08-287-717-6   | Sequence 6, Appl  |
| 27         | 26.5  | 44.2        | 14     | 1  | US-08-481-888A-16 | Sequence 16, Appl |

|    |      |      |    |   |                    |                   |
|----|------|------|----|---|--------------------|-------------------|
| 28 | 26.5 | 44.2 | 14 | 1 | US-08-485-273A-16  | Sequence 16, Appl |
| 29 | 26.5 | 44.2 | 14 | 1 | US-08-441-914-6    | Sequence 6, Appl  |
| 30 | 26.5 | 44.2 | 14 | 2 | US-08-973-563A-16  | Sequence 16, Appl |
| 31 | 26.5 | 44.2 | 14 | 2 | US-08-973-559-16   | Sequence 16, Appl |
| 32 | 25   | 41.7 | 12 | 1 | US-08-511-662-8    | Sequence 8, Appl  |
| 33 | 25   | 41.7 | 12 | 5 | PCT-US96-12632-8   | Sequence 8, Appl  |
| 34 | 24   | 40.0 | 8  | 3 | US-08-925-002-16   | Sequence 16, Appl |
| 35 | 24   | 40.0 | 8  | 4 | US-09-910-552-16   | Sequence 16, Appl |
| 36 | 24   | 40.0 | 9  | 1 | US-08-215-805A-41  | Sequence 41, Appl |
| 37 | 24   | 40.0 | 9  | 4 | US-09-417-608A-86  | Sequence 86, Appl |
| 38 | 24   | 40.0 | 10 | 1 | US-07-909-122-5    | Sequence 5, Appl  |
| 39 | 24   | 40.0 | 10 | 4 | US-08-135-319A-8   | Sequence 8, Appl  |
| 40 | 24   | 40.0 | 11 | 1 | US-08-269-441A-3   | Sequence 3, Appl  |
| 41 | 24   | 40.0 | 12 | 4 | US-09-446-787B-88  | Sequence 88, Appl |
| 42 | 24   | 40.0 | 12 | 4 | US-09-407-687-12   | Sequence 12, Appl |
| 43 | 24   | 40.0 | 13 | 2 | US-08-480-190-229  | Sequence 229, App |
| 44 | 24   | 40.0 | 13 | 2 | US-08-488-379-229  | Sequence 229, App |
| 45 | 24   | 40.0 | 13 | 4 | US-08-475-399A-229 | Sequence 229, App |

ALIGNMENTS

RESULT 1  
US-08-481-888A-19  
; Sequence 19, Application US/08481888A  
; Patent No. 5631228  
; GENERAL INFORMATION:  
; APPLICANT: Oppenheim, Frank G.  
; APPLICANT: Xu, Tao  
; TITLE OF INVENTION: ANTI-FUNGAL AND ANTI-BACTERIAL  
; TITLE OF INVENTION: HISTATIN-BASED PEPTIDES  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/481, 888A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/287, 717  
; FILING DATE: 09-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/145, 030  
; FILING DATE: 28-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/786, 571  
; FILING DATE: 01-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: PER95-01A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-481-888A-19

Query Match 44.2%; Score 26.5; DB 1; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 GYKNSKFH 8  
DB 5 GYKR-KFH 11

## RESULT 2

US-08-485-273A-19  
; Sequence 19, Application US/08485273A  
; Patent No. 5646119  
; GENERAL INFORMATION:  
; APPLICANT: Oppenheim, Frank G.  
; APPLICANT: Xu, Tao  
; APPLICANT: Spacciapoli, Peter  
; TITLE OF INVENTION: D-Amino Acid Histatin-Based Peptides as  
; TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial Agents  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,273A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/287,717  
; FILING DATE: 09-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/145,030  
; FILING DATE: 28-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/786,571  
; FILING DATE: 01-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: PER95-02A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 1..11  
; OTHER INFORMATION:  
; OTHER INFORMATION: /note= "At least one amino acid  
; must have a D configuration."  
; US-08-485-273A-19

Query Match 44.2%; Score 26.5; DB 1; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 GYKNSKFH 8

DB 5 GYKR-KFH 11

## RESULT 3

US-08-973-563A-19  
; Sequence 19, Application US/08973563A  
; Patent No. 5885965  
; GENERAL INFORMATION:  
; APPLICANT: Oppenheim, Frank G.  
; APPLICANT: Xu, Tao  
; APPLICANT: Spacciapoli, Peter  
; APPLICANT: Roberts, F. D.  
; APPLICANT: Friden, Philip M.  
; TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based  
; TITLE OF INVENTION: Peptides  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/973,563A  
; FILING DATE: 07-JUN-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,273  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: PER95-02A2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 781-861-6240  
; TELEFAX: 781-861-9540  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 1..11  
; OTHER INFORMATION:  
; OTHER INFORMATION: /note= "At least one amino acid  
; must have a D configuration."  
; US-08-973-563A-19

Query Match 44.2%; Score 26.5; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 GYKNSKFH 8  
DB 5 GYKR-KFH 11

## RESULT 4

US-08-973-559-19  
; Sequence 19, Application US/08973559  
; Patent No. 5912230  
; GENERAL INFORMATION:  
; APPLICANT: OPPENHEIM, FRANK G.  
; APPLICANT: XU, TAO

```

: APPLICANT: ROBERTS, F. D.
: APPLICANT: SPACCIAPOLI, PETER
: APPLICANT: FRIDEN, PHILIP M.
: TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
: TITLE OF INVENTION: Histatin-Based Peptides
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
: STREET: Two Militia Drive
: CITY: Lexington
: STATE: MA
: COUNTRY: US
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/973,559
: FILING DATE: 07-JUN-1996
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/481,888
: FILING DATE: 07-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Brook, David E.
: REGISTRATION NUMBER: 22,592
: REFERENCE/DOCKET NUMBER: PER95-01A2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 781-861-6240
: TELEFAX: 781-861-9540
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 11 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-973-559-19

Query Match 44.2%; Score 26.5; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYXNSKFH 8
Db 5 GYKR-KFH 11

RESULT 5
US-08-481-888A-18
: Sequence 18, Application US/08481888A
: Patent No. 5631228
: GENERAL INFORMATION:
: APPLICANT: Openheim, Frank G.
: APPLICANT: Xu, Tao
: APPLICANT: Roberts, F. Donald
: TITLE OF INVENTION: ANTI-FUNGAL AND ANTI-BACTERIAL
: TITLE OF INVENTION: HISTATIN-BASED PEPTIDES
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
: STREET: Two Militia Drive
: CITY: Lexington
: STATE: MA
: COUNTRY: US
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/481,888A
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/287,717
: FILING DATE: 09-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/145,030
: FILING DATE: 28-OCT-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/786,571
: FILING DATE: 01-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Brook, David E.
: REGISTRATION NUMBER: 22,592
: REFERENCE/DOCKET NUMBER: PER95-01A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-861-6240
: TELEFAX: 617-861-9540
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 12 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-481-888A-18

Query Match 44.2%; Score 26.5; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYXNSKFH 8
Db 6 GYKR-KFH 12

RESULT 6
US-08-485-273A-18
: Sequence 18, Application US/08485273A
: Patent No. 5646119
: GENERAL INFORMATION:
: APPLICANT: Openheim, Frank G.
: APPLICANT: Xu, Tao
: APPLICANT: Spacciapoli, Peter
: TITLE OF INVENTION: D-Amino Acid Histatin-Based Peptides as
: TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial Agents
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
: STREET: Two Militia Drive
: CITY: Lexington
: STATE: MA
: COUNTRY: US
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,273A
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/287,717
: FILING DATE: 09-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/145,030
: FILING DATE: 28-OCT-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/786,571
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FILING DATE: 01-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: PER95-02A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..12  
OTHER INFORMATION: /note= "At least one amino acid  
OTHER INFORMATION: must have a D configuration."  
US-08-485-273A-18

Query Match 44.2%; Score 26.5; DB 1; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8  
||| |||  
DB 6 GYKR-KFH 12

RESULT 7  
US-08-973-563A-18  
Sequence 18, Application US/08973563A  
Patent No. 5885965  
GENERAL INFORMATION:  
APPLICANT: Oppenheim, Frank G.  
APPLICANT: Xu, Tao  
APPLICANT: Spacciapoli, Peter  
APPLICANT: Roberts, F. D.  
APPLICANT: Friden, Philip M.  
TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based  
TITLE OF INVENTION: Peptides  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,563A  
FILING DATE: 07-JUN-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,273  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: PER95-02A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids

TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..12  
OTHER INFORMATION: /note= "At least one amino acid  
OTHER INFORMATION: must have a D configuration."  
US-08-973-563A-18

Query Match 44.2%; Score 26.5; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8  
||| |||  
DB 6 GYKR-KFH 12

RESULT 8  
US-08-973-563A-24  
Sequence 24, Application US/08973563A  
Patent No. 5885965  
GENERAL INFORMATION:  
APPLICANT: Oppenheim, Frank G.  
APPLICANT: Xu, Tao  
APPLICANT: Spacciapoli, Peter  
APPLICANT: Roberts, F. D.  
APPLICANT: Friden, Philip M.  
TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based  
TITLE OF INVENTION: Peptides  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,563A  
FILING DATE: 07-JUN-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,273  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: PER95-02A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..12  
OTHER INFORMATION: /note= "At least one amino acid  
OTHER INFORMATION: must have a D configuration."  
US-08-973-563A-24

Query Match 44.2%; Score 26.5; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKNSKFH 8  
Db 6 GYKR-KFH 12

## RESULT 9

US-08-973-563A-25  
Sequence 25, Application US/08973563A  
Patent No. 5885965  
GENERAL INFORMATION:  
APPLICANT: Oppenheim, Frank G.  
APPLICANT: Xu, Tao  
APPLICANT: Spacciapoli, Peter  
APPLICANT: Roberts, F. D.  
APPLICANT: Friden, Philip M.  
TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,563A  
FILING DATE: 07-JUN-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,273  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: PER95-02A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..12  
OTHER INFORMATION: /note= "At least one amino acid  
OTHER INFORMATION: must have a D configuration."  
US-08-973-563A-25

Query Match 44.2%; Score 26.5; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKNSKFH 8  
Db 6 GYKR-KFH 12

RESULT 10  
US-08-973-563A-27

Sequence 27, Application US/08973563A  
Patent No. 5885965  
GENERAL INFORMATION:

APPLICANT: Oppenheim, Frank G.

APPLICANT: Xu, Tao

APPLICANT: Spacciapoli, Peter

APPLICANT: Roberts, F. D.

APPLICANT: Friden, Philip M.

TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: US

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/973,563A

FILING DATE: 07-JUN-1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/485,273

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: PER95-02A2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240

TELEFAX: 781-861-9540

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Region

LOCATION: 1..12

OTHER INFORMATION: /note= "At least one amino acid

OTHER INFORMATION: must have a D configuration."  
US-08-973-563A-27

Query Match 44.2%; Score 26.5; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKNSKFH 8  
Db 6 GYKR-KFH 12

## RESULT 11

US-08-973-563A-36

Sequence 36, Application US/08973563A

Patent No. 5885965

GENERAL INFORMATION:

APPLICANT: Oppenheim, Frank G.

APPLICANT: Xu, Tao

APPLICANT: Spacciapoli, Peter

APPLICANT: Roberts, F. D.

APPLICANT: Friden, Philip M.

TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based

NUMBER OF SEQUENCES: 37

```

CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,563A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,273
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-02A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..12
OTHER INFORMATION: /note="At least one amino acid
OTHER INFORMATION: must have a D configuration."
US-08-973-563A-36

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKNSKPFH 8
Db 6 GYK-QKPFH 12

RESULT 12
US-08-973-559-18
Sequence 18, Application US/08973559
Patent No. 5912230
GENERAL INFORMATION:
APPLICANT: OPPENHEIM, FRANK G.
APPLICANT: XU, TAO
APPLICANT: ROBERTS, F. D.
APPLICANT: SPACCIAPOLI, PETER
APPLICANT: FRIDEN, PHILIP M.
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
TITLE OF INVENTION: Histatin-Based Peptides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,559
FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,888
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-01A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-973-559-18

Query Match 44.2%; Score 26.5; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 1,1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKNSKPH 8
||| |||
Db 6 GYKR-KFH 12

RESULT 13
US-08-973-559-24
Sequence 24, Application US/08973559
Patent No. 5912230
GENERAL INFORMATION:
APPLICANT: OPPENHEIM, FRANK G.
APPLICANT: XU, TAO
APPLICANT: ROBERTS, F. D.
APPLICANT: SPACCIAPOLI, PETER
APPLICANT: FRIDEN, PHILIP M.
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial
TITLE OF INVENTION: Histatin-Based Peptides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,559
FILING DATE: 07-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,888
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: PER95-01A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
INFORMATION FOR SEQ ID NO: 24:

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SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-973-559-24

Query Match 44.2%; Score 26.5; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 GYKSKFH 8  
||| |||  
DB 6 GYKR-KFH 12

RESULT 14  
US-08-973-559-25  
Sequence 25, Application US/08973559  
Patent No. 5912230  
GENERAL INFORMATION:  
APPLICANT: OPPENHEIM, FRANK G.  
APPLICANT: XU, TAO  
APPLICANT: ROBERTS, F. D.  
APPLICANT: SPACCIAPOLI, PETER  
APPLICANT: FRIDEN, PHILIP M.  
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,559  
FILING DATE: 07-JUN-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/481,888  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: PER95-01A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-973-559-25

Query Match 44.2%; Score 26.5; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
OY 1 GYKSKFH 8  
||| |||  
DB 6 GYKR-KFH 12

RESULT 15  
US-08-973-559-27  
Sequence 27, Application US/08973559  
Patent No. 5912230  
GENERAL INFORMATION:  
APPLICANT: OPPENHEIM, FRANK G.  
APPLICANT: XU, TAO  
APPLICANT: ROBERTS, F. D.  
APPLICANT: SPACCIAPOLI, PETER  
APPLICANT: FRIDEN, PHILIP M.  
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,559  
FILING DATE: 07-JUN-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/481,888  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: PER95-01A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-973-559-27

Query Match 44.2%; Score 26.5; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 GYKSKFH 8  
||| |||  
DB 6 GYKR-KFH 12

RESULT 16  
US-08-973-559-36  
Sequence 36, Application US/08973559  
Patent No. 5912230  
GENERAL INFORMATION:  
APPLICANT: OPPENHEIM, FRANK G.  
APPLICANT: XU, TAO  
APPLICANT: ROBERTS, F. D.  
APPLICANT: SPACCIAPOLI, PETER  
APPLICANT: FRIDEN, PHILIP M.  
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,559  
FILING DATE: 07-JUN-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/481,888  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: PER95-01A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-973-559-36

Query Match 44.2%; Score 26.5; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 GYKSKFH 8  
||| |||  
Db 6 GYK-QKFH 12

RESULT 17  
US-08-993-235-4  
; Sequence 4, Application US/08993235  
; Patent No. 6084064  
; GENERAL INFORMATION:  
; APPLICANT: OPPENHEIM, FRANK G.  
; APPLICANT: ROBERTS, F. DONALD  
; APPLICANT: XU, TAO  
; APPLICANT: SPACCIAPOLI, PETER  
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES  
; FILE REFERENCE: 50032/002001  
; CURRENT APPLICATION NUMBER: US/08/993,235  
; CURRENT FILING DATE: 1997-12-18  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-993-235-4

Query Match 44.2%; Score 26.5; DB 3; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 GYKSKFH 8  
||| |||  
Db 6 GYK-QKFH 12

RESULT 18

US-08-993-235-5  
; Sequence 5, Application US/08993235  
; Patent No. 6084064  
; GENERAL INFORMATION:  
; APPLICANT: OPPENHEIM, FRANK G.  
; APPLICANT: ROBERTS, F. DONALD  
; APPLICANT: XU, TAO  
; APPLICANT: SPACCIAPOLI, PETER  
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES  
; FILE REFERENCE: 50032/002001  
; CURRENT APPLICATION NUMBER: US/08/993,235  
; CURRENT FILING DATE: 1997-12-18  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-993-235-5

Query Match 44.2%; Score 26.5; DB 3; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 GYKSKFH 8  
||| |||  
Db 6 GYK-QKFH 12

RESULT 19  
US-08-993-235-7  
; Sequence 7, Application US/08993235  
; Patent No. 6084064  
; GENERAL INFORMATION:  
; APPLICANT: OPPENHEIM, FRANK G.  
; APPLICANT: ROBERTS, F. DONALD  
; APPLICANT: XU, TAO  
; APPLICANT: SPACCIAPOLI, PETER  
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES  
; FILE REFERENCE: 50032/002001  
; CURRENT APPLICATION NUMBER: US/08/993,235  
; CURRENT FILING DATE: 1997-12-18  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-993-235-7

Query Match 44.2%; Score 26.5; DB 3; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 GYKSKFH 8  
||| |||  
Db 6 GYK-QKFH 12

RESULT 20  
US-09-226-666-1  
; Sequence 1, Application US/09226666A  
; Patent No. 6528488  
; GENERAL INFORMATION:  
; APPLICANT: Spacciapoli, Peter  
; APPLICANT: Rotenstein, David M.  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS  
; FILE REFERENCE: 50032/007001  
; CURRENT APPLICATION NUMBER: US/09/226,666A  
; CURRENT FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Internal fragment
US-09-226-666-1
```

```
Query Match          44.2%; Score 26.5; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      1 GYKNSKFH 8
      ||| |||
Db      6 GYKR-KFH 12
```

## RESULT 21

```
US-09-226-666-13
; Sequence 13, Application US/09226666A
; Patent No. 6528488
; GENERAL INFORMATION:
; APPLICANT: Spacciapoli, Peter
; APPLICANT: Rothstein, David M.
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
; FILE REFERENCE: 50032/007001
; CURRENT APPLICATION NUMBER: US/09/226,666A
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from Homo sapiens
US-09-226-666-13
```

```
Query Match          44.2%; Score 26.5; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      1 GYKNSKFH 8
      ||| |||
Db      6 GYK-QKFH 12
```

## RESULT 22

```
US-09-226-666-16
; Sequence 16, Application US/09226666A
; Patent No. 6528488
; GENERAL INFORMATION:
; APPLICANT: Spacciapoli, Peter
; APPLICANT: Rothstein, David M.
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
; FILE REFERENCE: 50032/007001
; CURRENT APPLICATION NUMBER: US/09/226,666A
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from Homo sapiens
US-09-226-666-16
```

```
Query Match          44.2%; Score 26.5; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      1 GYKNSKFH 8
      ||| |||
Db      6 GYK-KKFH 12
```

## RESULT 23

```
US-08-993-235-4
; Sequence 4, Application US/08993235
; Patent No. 6531573
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993,235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-4
```

```
Query Match          44.2%; Score 26.5; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      1 GYKNSKFH 8
      ||| |||
Db      6 GYKR-KFH 12
```

## RESULT 24

```
US-08-993-235-5
; Sequence 5, Application US/08993235
; Patent No. 6531573
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
; APPLICANT: XU, TAO
; APPLICANT: SPACCIAPOLI, PETER
; TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES
; FILE REFERENCE: 50032/002001
; CURRENT APPLICATION NUMBER: US/08/993,235
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-993-235-5
```

```
Query Match          44.2%; Score 26.5; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      1 GYKNSKFH 8
      ||| |||
Db      6 GYKR-KFH 12
```

## RESULT 25

```
US-08-993-235-7
; Sequence 7, Application US/08993235
; Patent No. 6531573
; GENERAL INFORMATION:
; APPLICANT: OPPENHEIM, FRANK G.
; APPLICANT: ROBERTS, F. DONALD
```

APPLICANT: XU, TAO  
APPLICANT: SPACCIAPOLI, PETER  
TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES  
FILE REFERENCE: 50032/002001  
CURRENT APPLICATION NUMBER: US/08/993,235  
CURRENT FILING DATE: 1997-12-18  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 7  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-993-235-7

Query Match 44.2%; Score 26.5; DB 1; Length 12;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 GYKSKFH 8  
Db 6 GYKR-KFH 12

## RESULT 26

US-08-287-717-6  
Sequence 6, Application US/08287717  
Patent No. 5486503  
GENERAL INFORMATION:  
APPLICANT: Oppenheim, Frank G.  
TITLE OF INVENTION: No. 5486503e1 Anti-Fungal Peptides and Uses  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/287,717  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/145,030  
FILING DATE:  
APPLICATION NUMBER: US 07/786,571  
FILING DATE: 01-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: BU91-17  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-287-717-6

Query Match 44.2%; Score 26.5; DB 1; Length 14;  
Best Local Similarity 75.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 GYKSKFH 8  
Db 1 GYKR-KFH 7

## RESULT 27

US-08-481-888A-16  
Sequence 16, Application US/08481888A  
Patent No. 5631228  
GENERAL INFORMATION:  
APPLICANT: Oppenheim, Frank G.  
APPLICANT: Xu, Tao  
APPLICANT: Roberts, F. Donald  
TITLE OF INVENTION: ANTI-FUNGAL AND ANTI-BACTERIAL  
TITLE OF INVENTION: HISTATIN-BASED PEPTIDES  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,888A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/287,717  
FILING DATE: 09-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/145,030  
FILING DATE: 28-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/786,571  
FILING DATE: 01-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: PER95-01A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-481-888A-16

Query Match 44.2%; Score 26.5; DB 1; Length 14;  
Best Local Similarity 75.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 GYKSKFH 8  
Db 1 GYKR-KFH 7

## RESULT 28

US-08-485-273A-16  
Sequence 16, Application US/08485273A  
Patent No. 5646119  
GENERAL INFORMATION:  
APPLICANT: Oppenheim, Frank G.  
APPLICANT: Xu, Tao

APPLICANT: Spacciapoli, Peter  
TITLE OF INVENTION: D-Amino Acid Histatin-Based Peptides as  
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial Agents  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,273A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/287,717  
FILING DATE: 09-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/145,030  
FILING DATE: 28-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/786,571  
FILING DATE: 01-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: PER95-02A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..14  
OTHER INFORMATION: /note="At least one amino acid  
OTHER INFORMATION: must have a D configuration."  
US-08-485-273A-16

Query Match 44.2%; Score 26.5; DB 1; Length 14;  
Best Local Similarity 75.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8  
||| |||  
Db 1 GYKR-KFH 7

RESULT 29  
US-08-441-914-6  
Sequence 6, Application US/08441914  
Patent No. 5696078  
GENERAL INFORMATION:  
APPLICANT: Oppenheim, Frank G.  
APPLICANT: Xu, Tao  
TITLE OF INVENTION: No. 5696078e1 Anti-Fungal Peptides and Uses  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington

STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,914  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/287,717  
FILING DATE: 09-AUG-94  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/145,030  
FILING DATE: 28-OCT-93  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/786,571  
FILING DATE: 01-NOV-91  
ATTORNEY/AGENT INFORMATION:  
NAME: David E. Brook  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: BU91-17F22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-441-914-6

Query Match 44.2%; Score 26.5; DB 1; Length 14;  
Best Local Similarity 75.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GYKSKFH 8  
||| |||  
Db 1 GYKR-KFH 7

RESULT 30  
US-08-973-563A-16  
Sequence 16, Application US/08973563A  
Patent No. 5885965  
GENERAL INFORMATION:  
APPLICANT: Oppenheim, Frank G.  
APPLICANT: Xu, Tao  
APPLICANT: Spacciapoli, Peter  
APPLICANT: Roberts, F. D.  
APPLICANT: Friden, Philip M.  
TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based  
TITLE OF INVENTION: Peptides  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,563A  
FILING DATE: 07-JUN-1996

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,273  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: PER95-02A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..14  
OTHER INFORMATION: /note= "At least one amino acid  
OTHER INFORMATION: must have a D configuration."  
US-08-973-563A-16

Query Match 44.2%; Score 26.5; DB 2; Length 14;  
Best Local Similarity 75.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 1 GYKSKFH 8  
Db 1 GYKR-KFH 7

RESULT 31  
US-08-973-559-16  
Sequence 16, Application US/08973559  
Patent No. 5912230  
GENERAL INFORMATION:  
APPLICANT: OPPENHEIM, FRANK G.  
APPLICANT: XU, TAO  
APPLICANT: ROBERTS, F. D.  
APPLICANT: SPACCIAPOLI, PETER  
APPLICANT: FRIDEN, PHILIP M.  
TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial  
TITLE OF INVENTION: Histatin-Based Peptides  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,559  
FILING DATE: 07-JUN-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/481,888  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: PER95-01A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-973-559-16

Query Match 44.2%; Score 26.5; DB 2; Length 14;  
Best Local Similarity 75.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 1 GYKSKFH 8  
Db 1 GYKR-KFH 7

RESULT 32  
US-08-511-662-8  
Sequence 8, Application US/08511662  
Patent No. 5807552  
GENERAL INFORMATION:  
APPLICANT: Stanton, G. John  
APPLICANT: Hughes, Jr., Thomas K.  
APPLICANT: Smith, Eric M.  
TITLE OF INVENTION: Compositions for Conferring Immunogenicity  
TITLE OF INVENTION: to a Substance and Uses Thereof  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/511,662  
FILING DATE: Concurrently herewith  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Hodgins, Daniel S.  
REGISTRATION NUMBER: 31,026  
REFERENCE/DOCKET NUMBER: UTSG:162/HOD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 515/418-3000  
TELEFAX: 512/474-7577  
TELEX: NA  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-511-662-8

Query Match 41.7%; Score 25; DB 1; Length 12;  
Best Local Similarity 57.1%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKSKFH 8  
Db 5 YLNLRFH 11

RESULT 33  
PCT-US96-12632-8

```
; Sequence 8, Application PC/TUS9612632
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT: NAME: BOARD OF REGENTS, THE UNIVERSITY OF
; APPLICANT: TEXAS SYSTEM
; APPLICANT: STREET: 201 West 7th Street
; APPLICANT: CITY: Austin
; APPLICANT: STATE: Texas
; APPLICANT: COUNTRY: United States of America
; APPLICANT: POSTAL CODE: 78701
; APPLICANT: TELEPHONE NO: (512) 499-4462
; APPLICANT: TELEFAX: (512) 499-4523
; TITLE OF INVENTION: COMPOSITIONS FOR CONFERRING
; TITLE OF INVENTION: IMMUNOGENICITY TO A SUBSTANCE AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12632
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/511,662
; FILING DATE: 04 August 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: HODGINS, DANIEL S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UFG162P--
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 515/418-3000
; TELEFAX: 512/474-7577
; TELEX: NA
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US96-12632-8

Query Match 41.7%; Score 25; DB 5; Length 12;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 YKNSKPFH 8
DB 5 YLNRFRH 11

RESULT 34
US-08-925-002-16
; Sequence 16, Application US/08925002
; Patent No. 6048527
; GENERAL INFORMATION:
; APPLICANT: Granoff, Dan M.
; APPLICANT: Moe, Gregory R.
; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
; FILE REFERENCE: 1238.002
```

```
; CURRENT APPLICATION NUMBER: US/08/925,002
; CURRENT FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence from
; US-08-925-002-16

Query Match 40.0%; Score 24; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 GYKNSKPFH 8
DB 1 GYEVQPFH 8

RESULT 35
US-09-910-552-16
; Sequence 16, Application US/09910552
; Patent No. 6642354
; GENERAL INFORMATION:
; APPLICANT: Granoff, Dan M.
; APPLICANT: Moe, Gregory R.
; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
; FILE REFERENCE: 1238.002
; CURRENT APPLICATION NUMBER: US/09/910,552
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 09/494,822
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence from
; US-09-910-552-16

Query Match 40.0%; Score 24; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 GYKNSKPFH 8
DB 1 GYEVQPFH 8

RESULT 36
US-08-215-805A-41
; Sequence 41, Application US/08215805A
; Patent No. 5559008
; GENERAL INFORMATION:
; APPLICANT: Chang, Yung-Fu
; TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTURELLA
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
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## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/215,805A  
FILING DATE: 22-MAR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Timian, Susan J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1636  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Actinobacillus pleuropneumoniae  
US-08-215-805A-41

Query Match 40.0%; Score 24; DB 1; Length 9;  
Best Local Similarity 44.4%; Pred. No. 3e+05;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKNSKFHRV 10  
: ||||| :  
Db 1 FKGSKFRDI 9

## RESULT 37

US-09-417-608A-86  
Sequence 86, Application US/09417608A  
Patent No. 6686164  
GENERAL INFORMATION:  
APPLICANT: Olsen, Arne  
APPLICANT: Røsgen, Erwin  
APPLICANT: Ernst, Steffen  
TITLE OF INVENTION: Low Allergenic Protein Variants  
FILE REFERENCE: 5676.200-US  
CURRENT APPLICATION NUMBER: US/09/417,608A  
CURRENT FILING DATE: 1999-10-13  
NUMBER OF SEQ ID NOS: 101  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 86  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-417-608A-86

Query Match 40.0%; Score 24; DB 4; Length 9;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YKNSKF 7  
: ||||| :  
Db 3 FSNKSF 8

## RESULT 38

US-07-909-122-5  
Sequence 5, Application US/07909122  
Patent No. 5415995  
GENERAL INFORMATION:  
APPLICANT: SCHOOLNIK, GARY K.

APPLICANT: PALEFSKY, JOEL M.  
TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA  
VIRUS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/909,122  
FILING DATE: 19920706  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: BENZ, WILLIAM H.  
REGISTRATION NUMBER: 25,952  
REFERENCE/DOCKET NUMBER: 28600-20105.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-909-122-5

Query Match 40.0%; Score 24; DB 1; Length 10;  
Best Local Similarity 37.5%; Pred. No. 2.6e+02;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSKFHRV 10  
: ||||| :  
Db 2 KKQRFHNI 9 /

## RESULT 39

US-08-135-319A-8  
Sequence 8, Application US/08135319A  
Patent No. 6528487  
GENERAL INFORMATION:  
APPLICANT: Heaven, George A.  
APPLICANT: McBever, Rodger P.  
APPLICANT: Geng, Jian-Guo  
TITLE OF INVENTION: Peptide Inhibitors of Inflammation Mediated by Selectins  
FILE REFERENCE: CTC 102 CON  
CURRENT APPLICATION NUMBER: US/08/135,319A  
CURRENT FILING DATE: 1993-10-12  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 8  
LENGTH: 10  
TYPE: PRT  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic inhibitory peptide  
US-08-135-319A-8

Query Match 40.0%; Score 24; DB 4; Length 10;  
Best Local Similarity 80.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKNSK 6  
: ||||| :  
Db 2 YKNSK 6



Db 1 YKNNK 5

## RESULT 40

US-08-269-441A-3  
; Sequence 3, Application US/08269441A  
; Patent No. 5552529  
; GENERAL INFORMATION:  
; APPLICANT: Rearden, Ann  
; TITLE OF INVENTION: A NOVEL AUTOANTIGEN, PINCH  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/269,441A  
; FILING DATE: 30-JUN-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile Ph.D., Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07257/009001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 678-5070  
; TELEFAX: (619) 678-5099  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..11  
; US-08-269-441A-3

Query Match 40.0%; Score 24; DB 1; Length 11;  
Best Local Similarity 42.9%; Pred. No. 2.8e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKNSKPFH 8  
:|:|:  
Db 1 FKNDPYH 7

## RESULT 41

US-09-446-787B-88  
; Sequence 88, Application US/09446787B  
; Patent No. 6541198  
; GENERAL INFORMATION:  
; APPLICANT: Akzo No. 6541198el N.V.  
; APPLICANT: Paulij, Wilhemina P.  
; APPLICANT: Van Kessel-Koens, Marjolijn J.  
; TITLE OF INVENTION: Antibodies and other binding molecules specific for hepatitis B  
; TITLE OF INVENTION: antigens  
; FILE REFERENCE: 9310-19  
; CURRENT APPLICATION NUMBER: US/09/446,787B  
; CURRENT FILING DATE: 2000-01-13  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 88  
; LENGTH: 12  
; TYPE: PRT

; ORGANISM: Hepatitis B virus  
US-09-446-787B-88

Query Match 40.0%; Score 24; DB 4; Length 12;  
Best Local Similarity 30.0%; Pred. No. 3.1e+02;  
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKNSKPFHRY 11  
:|:|:|:  
Db 3 WNSTTFHQVL 12

## RESULT 42

US-09-407-687-12  
; Sequence 12, Application US/09407687  
; Patent No. 6548634  
; GENERAL INFORMATION:  
; APPLICANT: Ballinger, Marcus  
; APPLICANT: Kavanaugh, Michael  
; TITLE OF INVENTION: Synthetic Peptides Having FGF Receptor  
; TITLE OF INVENTION: Affinity  
; FILE REFERENCE: 1517.001  
; CURRENT APPLICATION NUMBER: US/09/407,687  
; CURRENT FILING DATE: 1999-09-28  
; EARLIER APPLICATION NUMBER: 60/102,667  
; EARLIER FILING DATE: 1998-09-30  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSEQ for windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
; US-09-407-687-12

Query Match 40.0%; Score 24; DB 4; Length 12;  
Best Local Similarity 50.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYKNSKPFH 8  
||:|:  
Db 5 GYYSCTFH 12

## RESULT 43

US-08-480-190-229  
; Sequence 229, Application US/08480190  
; Patent No. 5827516  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Urban  
; APPLICANT: Roman M. ChicZ  
; APPLICANT: Dario A. A. Vignali  
; APPLICANT: Mary L. Hedley  
; APPLICANT: Lawrence J. Stern  
; APPLICANT: Jack L. Strominger  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,190  
; FILING DATE:

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 229:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-480-190-229

Query Match 40.0%; Score 24; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 3.4e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKSKFHRV 10  
|:| |:  
DB 5 YRGSTSHRL 13

RESULT 44  
US-08-488-379-229  
Sequence 229, Application US/08488379  
Patent No. 5880103  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 50Z or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,379  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 229:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-488-379-229

Query Match 40.0%; Score 24; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 3.4e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKSKFHRV 10  
|:| |:  
DB 5 YRGSTSHRL 13

RESULT 45  
US-08-475-399A-229  
Sequence 229, Application US/08475399A  
Patent No. 6509033  
GENERAL INFORMATION:  
APPLICANT: Urban, Robert G.  
APPLICANT: Chicz, Roman M.  
APPLICANT: Vignali, Dario A.A.  
APPLICANT: Hedley, Mary L.  
APPLICANT: Stern, Lawrence J.  
APPLICANT: Strominger, Jack L.  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 276  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,399A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: 15-JUN-1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: 11-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00246/168003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-507  
TELEFAX: 617/542-890  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 229:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-475-399A-229

Query Match 40.0%; Score 24; DB 4; Length 13;  
Best Local Similarity 44.4%; Pred. No. 3.4e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 YKSKFHRV 10  
|:| |:  
DB 5 YRGSTSHRL 13

Thu Sep 2 07:41:36 2004

Search completed: August 30, 2004, 10:57:13  
Job time : 5.34797 secs

us-09-720-469a-4.aug30.ra1

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 10.5912 Seconds  
(without alignments)  
327.696 Million cell updates/sec

Title: US-09-720-469A-5  
Perfect score: 71  
Sequence: 1 NFKLKHYPGW 11

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3347

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- SPTREMBL 25:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phage:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_virus:\*
  - 16: sp\_bacteriap:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID     | Description         |
|------------|-------|-------------|--------|----|--------|---------------------|
| 1          | 26    | 36.6        | 10     | 11 | Q9QVE9 | Q9qve9 mus sp. pro  |
| 2          | 26    | 36.6        | 12     | 10 | Q93YC8 | Q93yc8 nicotiana t  |
| 3          | 24    | 33.8        | 9      | 4  | Q9H326 | Q9h326 homo sapien  |
| 4          | 24    | 33.8        | 9      | 13 | Q9PRJ4 | Q9prj4 lepisosteus  |
| 5          | 24    | 33.8        | 12     | 8  | Q9XNR6 | Q9xnr6 pyraliella l |
| 6          | 24    | 33.8        | 12     | 15 | O12090 | O12090 caprine art  |
| 7          | 24    | 33.8        | 12     | 15 | O12094 | O12094 caprine art  |
| 8          | 24    | 33.8        | 12     | 15 | O12114 | O12114 caprine art  |
| 9          | 24    | 33.8        | 12     | 15 | O12082 | O12082 caprine art  |
| 10         | 24    | 33.8        | 12     | 15 | O12106 | O12106 caprine art  |
| 11         | 24    | 33.8        | 12     | 15 | O12092 | O12092 caprine art  |
| 12         | 24    | 33.8        | 12     | 15 | O12108 | O12108 caprine art  |
| 13         | 24    | 33.8        | 12     | 15 | O12074 | O12074 caprine art  |
| 14         | 24    | 33.8        | 12     | 15 | O12116 | O12116 caprine art  |
| 15         | 24    | 33.8        | 12     | 15 | O12118 | O12118 caprine art  |
| 16         | 24    | 33.8        | 12     | 15 | O12110 | O12110 caprine art  |

|    |    |      |    |    |        |                    |
|----|----|------|----|----|--------|--------------------|
| 17 | 24 | 33.8 | 12 | 15 | O12112 | O12112 caprine art |
| 18 | 24 | 33.8 | 12 | 15 | O12076 | O12076 caprine art |
| 19 | 24 | 33.8 | 12 | 15 | O12088 | O12088 caprine art |
| 20 | 24 | 33.8 | 12 | 15 | O12078 | O12078 caprine art |
| 21 | 24 | 33.8 | 12 | 15 | O12080 | O12080 caprine art |
| 22 | 24 | 33.8 | 12 | 15 | O12084 | O12084 caprine art |
| 23 | 24 | 33.8 | 12 | 15 | O12086 | O12086 caprine art |
| 24 | 22 | 31.0 | 8  | 8  | Q34909 | Q34909 locusta mig |
| 25 | 22 | 31.0 | 14 | 7  | Q8MH06 | Q8mh06 homo sapien |
| 26 | 22 | 31.0 | 14 | 7  | Q8MH35 | Q8mh35 homo sapien |
| 27 | 22 | 31.0 | 14 | 7  | Q8MH39 | Q8mh39 homo sapien |
| 28 | 22 | 31.0 | 14 | 7  | Q8MH18 | Q8mh18 homo sapien |
| 29 | 22 | 31.0 | 14 | 7  | Q8MH55 | Q8mh55 homo sapien |
| 30 | 22 | 31.0 | 14 | 7  | Q8MH40 | Q8mh40 homo sapien |
| 31 | 22 | 31.0 | 14 | 7  | Q8MH07 | Q8mh07 homo sapien |
| 32 | 22 | 31.0 | 14 | 7  | Q8MH04 | Q8mh04 homo sapien |
| 33 | 22 | 31.0 | 14 | 7  | Q8MH52 | Q8mh52 homo sapien |
| 34 | 22 | 31.0 | 14 | 7  | Q8MH26 | Q8mh26 homo sapien |
| 35 | 22 | 31.0 | 14 | 7  | Q8MH53 | Q8mh53 homo sapien |
| 36 | 22 | 31.0 | 14 | 7  | Q8MH20 | Q8mh20 homo sapien |
| 37 | 22 | 31.0 | 14 | 7  | Q8MH27 | Q8mh27 homo sapien |
| 38 | 22 | 31.0 | 14 | 7  | Q8MH05 | Q8mh05 homo sapien |
| 39 | 22 | 31.0 | 14 | 7  | Q8MH16 | Q8mh16 homo sapien |
| 40 | 22 | 31.0 | 14 | 7  | Q8MH38 | Q8mh38 homo sapien |
| 41 | 22 | 31.0 | 14 | 7  | Q8MH56 | Q8mh56 homo sapien |
| 42 | 22 | 31.0 | 14 | 7  | Q8MH14 | Q8mh14 homo sapien |
| 43 | 22 | 31.0 | 14 | 7  | Q8MH31 | Q8mh31 homo sapien |
| 44 | 22 | 31.0 | 14 | 7  | Q8MH30 | Q8mh30 homo sapien |
| 45 | 22 | 31.0 | 14 | 7  | Q8MH51 | Q8mh51 homo sapien |

ALIGNMENTS

|  |   |                    |        |            |    |        |
|--|---|--------------------|--------|------------|----|--------|
| RESULT 1   |   |                    |        |            |    |        |
| Q9QVE9   |   | PRELIMINARY;       | PRT;   | 10 AA.     |    |        |
| AC Q9QVE9;   |   |                    |        |            |    |        |
| DT 01-MAY-2000 (Tremblrel. 13, Created)                                |   |                    |        |            |    |        |
| DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)                   |   |                    |        |            |    |        |
| DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)                 |   |                    |        |            |    |        |
| DE Protamine MP2 intermediate protein PMP2/11 (Fragment).              |   |                    |        |            |    |        |
| OS Mus sp.   |   |                    |        |            |    |        |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |   |                    |        |            |    |        |
| OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  |   |                    |        |            |    |        |
| OX NCBI_TaxID=10095;   |   |                    |        |            |    |        |
| RN [1]   |   |                    |        |            |    |        |
| RP SEQUENCE.   |   |                    |        |            |    |        |
| RX MEDLINE=92174934; PubMed=1541289;                                   |   |                    |        |            |    |        |
| RA Chauviere M., Martinage A., Debarle M., Sautiere P., Chevallier F.; |   |                    |        |            |    |        |
| RT "Molecular characterization of six intermediate proteins in the     |   |                    |        |            |    |        |
| RT processing of mouse protamine P2 precursor."                        |   |                    |        |            |    |        |
| RL Eur. J. Biochem. 204:759-765(1992).                                 |   |                    |        |            |    |        |
| FT NON_TER   | 1                                       |                    |        |            |    |        |
| FT NON_TER   | 10                                      |                    |        |            |    |        |
| FT NON_TER   | 10                                      |                    |        |            |    |        |
| SQ SEQUENCE  | 10 AA; 1029 MW; FCAD2DD8676866D1 CRC64; |                    |        |            |    |        |
| Query Match  | 36.6%;                                  | Score 26;          | DB 11; | Length 10; |    |        |
| Best Local Similarity  | 80.0%;                                  | Pred. No. 8.2e+02; |        |            |    |        |
| Matches  | 4;                                      | Conservative       | 0;     | Mismatches | 1; | Indels |
|  |   |                    |        |            | 0; | Gaps   |
|  |   |                    |        |            |    | 0;     |
| QY   | 6 HYPG 10                               |                    |        |            |    |        |
| DB   | 3 HGGPG 7                               |                    |        |            |    |        |
| RESULT 2   |   |                    |        |            |    |        |
| Q93YC8   |   | PRELIMINARY;       | PRT;   | 12 AA.     |    |        |
| AC Q93YC8;   |   |                    |        |            |    |        |
| DT 01-DEC-2001 (Tremblrel. 19, Created)                                |   |                    |        |            |    |        |
| DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)                   |   |                    |        |            |    |        |
| DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)                 |   |                    |        |            |    |        |

DE Putative coat protein (Fragment).  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA van der Winden J.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20027532; PubMed=10557305;  
RA Jakowitsch J., Mette M.F., van der Winden J., Matzke M.A.,  
RA Matzke A.J.;  
RT "Integrated pararetroviral sequences define a unique class of  
RT dispersed repetitive DNA in plants";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:13241-13246(1999).  
DR EMBL: AJ414170; CAC88799.1; -.  
DR GO: GO:0019028; C: viral capsid; IEA.  
DR GO: GO:0005198; F: structural molecule activity; IEA.  
KM Coat protein.  
FT NON TER  
SQ SEQUENCE 12 AA; 1402 MW; 89226B3A0351E321 CRC64;  
  
Query Match  
Best Local Similarity 36.6%; Score 26; DB 10; Length 12;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 KHYG 8  
Db 6 KHYG 9  
  
RESULT 3  
Q9H326 PRELIMINARY; PRT; 9 AA.  
AC Q9H326;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)  
DE NAD+-dependent isocitrate dehydrogenase 3 alpha subunit  
DE (Fragment).  
GN IDH3A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kim Y.-O., Koh H.-J., Jo S.-H., Son M.-K., Huh T.-L.;  
RT "Structural and functional characterization of the human NAD+-  
RT dependent isocitrate dehydrogenase alpha subunit promoter";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF157515; AAG43379.1; -.  
FT NON TER  
SQ SEQUENCE 9 AA; 960 MW; C91CB0437DC7687D CRC64;  
  
Query Match  
Best Local Similarity 33.8%; Score 24; DB 4; Length 9;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 GPGW 11  
Db 3 GPGW 6  
  
RESULT 4  
Q9PRJ4 PRELIMINARY; PRT; 9 AA.  
AC Q9PRJ4;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
DE Bradykinin.  
OS Lepisosteus osseus (Long-nosed gar), and  
OS Amia calva (Bowfin).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;  
OC Lepisosteus.  
OX NCBI\_TaxID=34771, 7924;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95380361; PubMed=7651903;  
RA Conlon J.M., Platzack B., Maira L.E., Youson J.H., Olson K.R.;  
RT "Isolation and biological activity of [Trp5]bradykinin from the plasma  
RT of the phylogenetically ancient fish, the bowfin and the longnosed  
RT gar";  
RL peptides 16:485-489(1995).  
SQ SEQUENCE 9 AA; 1099 MW; 3393D775A3786777 CRC64;  
  
Query Match  
Best Local Similarity 33.8%; Score 24; DB 13; Length 9;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 PGM 11  
Db 3 PGM 5  
  
RESULT 5  
Q9XNR6 PRELIMINARY; PRT; 12 AA.  
AC Q9XNR6;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)  
DE NADH:ubiquinone oxidoreductase subunit 3 (Fragment).  
GN NAD3.  
OS Pyraliella littoralis.  
OC Mitochondrion.  
OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;  
OC Acinetosporaceae; Pyraliella.  
OX NCBI\_TaxID=2885;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=roscoff;  
RX MEDLINE=99346148; PubMed=10415341;  
RA Oudot M.P., Kloareg B., Loiseaux-de Goer S.;  
RT "The mitochondrial Pyraliella littoralis nad1 gene contains only the  
RL N-terminal Fes-binding domain";  
RL Gene 235:131-137(1999).  
DR EMBL: AF110139; AAD44051.1; -.  
DR GO: GO:0005739; C: mitochondrion; IEA.  
KM Mitochondrion; Ubiquinone.  
FT NON TER  
SQ SEQUENCE 12 AA; 1501 MW; 49750746424B5B13 CRC64;  
  
Query Match  
Best Local Similarity 33.8%; Score 24; DB 8; Length 12;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FKLKHYGP 9  
Db 2 FKLKHYGP 9  
  
RESULT 6  
O12090 PRELIMINARY; PRT; 12 AA.  
AC O12090;  
DT 01-JUL-1997 (TREMBlrel. 04, Created)  
DT 01-JUL-1997 (TREMBlrel. 04, last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)  
DE Tat protein (Fragment).  
GN TAT.

OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81436; AAB60826.1; -.  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lentiviral\_Tat.  
DR Pfam; PF02998; Lentiviral\_Tat; I.  
FT NON\_TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11  
|||  
Db 8 PGW 10

RESULT 7  
ID 012094 PRELIMINARY; PRT; 12 AA.  
AC 012094;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81438; AAB60830.1; -.  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lentiviral\_Tat.  
DR Pfam; PF02998; Lentiviral\_Tat; I.  
FT NON\_TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11  
|||  
Db 8 PGW 10

RESULT 8  
ID 012114 PRELIMINARY; PRT; 12 AA.  
AC 012114;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11660;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81448; AAB60850.1; -.  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lentiviral\_Tat.  
DR Pfam; PF02998; Lentiviral\_Tat; I.  
FT NON\_TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11  
|||  
Db 8 PGW 10

RESULT 9  
ID 012082 PRELIMINARY; PRT; 12 AA.  
AC 012082;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81432; AAB60818.1; -.  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lentiviral\_Tat.  
DR Pfam; PF02998; Lentiviral\_Tat; I.  
FT NON\_TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11  
|||  
Db 8 PGW 10

RESULT 10  
ID 012106 PRELIMINARY; PRT; 12 AA.  
AC 012106;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;

RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G to A substitutions.";  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U81444; AAB60842.1; -.  
 DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
 DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
 DR InterPro; IPR004247; LentiViral\_Tat.  
 DR Pfam; PF02998; LentiViral\_Tat; I.  
 FT NON TER 1  
 SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;  
 Query Match 33.8%; Score 24; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 PGW 11  
 Db 8 PGW 10

RESULT 11

ID 012092 PRELIMINARY; PRT; 12 AA.  
 AC 012092;  
 DT 01-JUL-1997 (TReMBLrel. 04, Created)  
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Tat protein (Fragment).  
 GN TAT.  
 OS Caprine arthritis encephalitis virus (CAEV).  
 OC Viruses; Retrovirdae; Retroviridae; LentiVirus.  
 OX NCBI\_TaxID=11660;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
 RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G to A substitutions.";  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U81437; AAB60828.1; -.  
 DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
 DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
 DR InterPro; IPR004247; LentiViral\_Tat.  
 DR Pfam; PF02998; LentiViral\_Tat; I.  
 FT NON TER 1  
 SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;  
 Query Match 33.8%; Score 24; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 PGW 11  
 Db 8 PGW 10

RESULT 12

ID 012108 PRELIMINARY; PRT; 12 AA.  
 AC 012108;  
 DT 01-JUL-1997 (TReMBLrel. 04, Created)  
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Tat protein (Fragment).  
 GN TAT.  
 OS Caprine arthritis encephalitis virus (CAEV).  
 OC Viruses; Retrovirdae; Retroviridae; LentiVirus.  
 OX NCBI\_TaxID=11660;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
 RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G to A substitutions.";  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U81445; AAB60844.1; -.  
 DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
 DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
 DR InterPro; IPR004247; LentiViral\_Tat.  
 DR Pfam; PF02998; LentiViral\_Tat; I.  
 FT NON TER 1  
 SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;  
 Query Match 33.8%; Score 24; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 PGW 11  
 Db 8 PGW 10

RESULT 13

ID 012074 PRELIMINARY; PRT; 12 AA.  
 AC 012074;  
 DT 01-JUL-1997 (TReMBLrel. 04, Created)  
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Tat protein (Fragment).  
 GN TAT.  
 OS Caprine arthritis encephalitis virus (CAEV).  
 OC Viruses; Retrovirdae; Retroviridae; LentiVirus.  
 OX NCBI\_TaxID=11660;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
 RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G to A substitutions.";  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U81428; AAB60810.1; -.  
 DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
 DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
 DR InterPro; IPR004247; LentiViral\_Tat.  
 DR Pfam; PF02998; LentiViral\_Tat; I.  
 FT NON TER 1  
 SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;  
 Query Match 33.8%; Score 24; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 PGW 11  
 Db 8 PGW 10

RESULT 14

ID 012116 PRELIMINARY; PRT; 12 AA.  
 AC 012116;  
 DT 01-JUL-1997 (TReMBLrel. 04, Created)  
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Tat protein (Fragment).  
 GN TAT.  
 OS Caprine arthritis encephalitis virus (CAEV).  
 OC Viruses; Retrovirdae; Retroviridae; LentiVirus.  
 OX NCBI\_TaxID=11660;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
 RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G to A substitutions.";  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U81449; AAB60852.1; -.  
 DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
 DR GO; GO:0045941; P:positive regulation of transcription; IEA.



DR InterPro; IPR004247; Lentiviral Tat.  
DR Pfam; PF02998; Lentiviral\_Tat; I.  
FT NON TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11  
|||  
Db 8 PGW 10

## RESULT 15

ID 012118 PRELIMINARY; PRT; 12 AA.  
AC 012118;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81450; AAB60854.1; -  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lentiviral Tat.  
DR Pfam; PF02998; Lentiviral\_Tat; I.  
FT NON TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11  
|||  
Db 8 PGW 10

## RESULT 16

ID 012110 PRELIMINARY; PRT; 12 AA.  
AC 012110;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81446; AAB60846.1; -  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lentiviral Tat.  
DR Pfam; PF02998; Lentiviral\_Tat; I.  
FT NON TER 1

SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11  
|||  
Db 8 PGW 10

## RESULT 17

ID 012112 PRELIMINARY; PRT; 12 AA.  
AC 012112;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81447; AAB60848.1; -  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lentiviral Tat.  
DR Pfam; PF02998; Lentiviral\_Tat; I.  
FT NON TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11  
|||  
Db 8 PGW 10

## RESULT 18

ID 012076 PRELIMINARY; PRT; 12 AA.  
AC 012076;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81429; AAB60812.1; -  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lentiviral Tat.  
DR Pfam; PF02998; Lentiviral\_Tat; I.  
FT NON TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11  
|||  
Db 8 PGW 10

RESULT 19

012088 PRELIMINARY; PRT; 12 AA.  
AC 012088;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCB1\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81435; AAB60824.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 12 AA; 1279 MW; 4B90BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11  
|||  
Db 8 PGW 10

RESULT 20

012078 PRELIMINARY; PRT; 12 AA.  
AC 012078;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCB1\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81430; AAB60814.1; -.  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; LentiViral\_Tat.  
DR Pfam; PF02998; LentiViral\_Tat; 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11  
|||  
Db 8 PGW 10

RESULT 21

012080 PRELIMINARY; PRT; 12 AA.  
AC 012080;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCB1\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81431; AAB60816.1; -.  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; LentiViral\_Tat.  
DR Pfam; PF02998; LentiViral\_Tat; 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11  
|||  
Db 8 PGW 10

RESULT 22

012084 PRELIMINARY; PRT; 12 AA.  
AC 012084;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCB1\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81433; AAB60820.1; -.  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; LentiViral\_Tat.  
DR Pfam; PF02998; LentiViral\_Tat; 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11  
|||  
Db 8 PGW 10

RESULT 23

012086

ID 012086 PRELIMINARY; PRT; 12 AA.  
AC 012086;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RT Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
RL EMBL; U81434; AAB60822.1; -  
DR EMBL; U81434; AAB60822.1; -  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lentiviral Tat.  
DR Pfam; PF02998; Lentiviral\_Tat; I.  
FT NON TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E864EB7 CRC64;

Query Match 33.8%; Score 24; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KGM 11  
Db 8 KGM 10

## RESULT 24

Q34909 PRELIMINARY; PRT; 8 AA.

ID 034909  
AC 034909;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Cytochrome b (Fragment).  
OS Locusta migratoria (Migratory locust).  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88223478; PubMed=2836084;  
RA McCracken A., Uhlenbusch I., Gellissen G.;  
RT "Structure of the cloned locusta migratoria mitochondrial genome:  
restriction mapping and sequence of its ND-1 (URF-1) gene.";  
RL Curr. Genet. 11:625-630(1987).  
DR EMBL; X05286; CAA28905.1; -  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1  
FT NON TER 8  
SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;

Query Match 31.0%; Score 22; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLM 6  
Db 5 KLM 8

RESULT 25  
Q8MH06 PRELIMINARY; PRT; 14 AA.  
ID Q8MH06

AC Q8MH06;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "A new splicing acceptor site and polyadenylation sequence signal  
RT contribute to increase the extraordinary diversity of DQA1 mRNA  
RT isoforms.";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' untranslated region.";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF533934; AAM94848.1; -  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1435 MW; C5E8A0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;  
Best Local Similarity 60.0%; Pred. No. 5.5e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYG 9  
Db 9 RHGP 13

## RESULT 26

Q8MH35 PRELIMINARY; PRT; 14 AA.

ID 08MH35  
AC 08MH35;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "A new splicing acceptor site and polyadenylation sequence signal  
RT contribute to increase the extraordinary diversity of DQA1 mRNA  
RT isoforms.";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' untranslated region.";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF533905; AAM94819.1; -  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1435 MW; C5E8A0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;  
Best Local Similarity 60.0%; Pred. No. 5.5e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYG 9  
Db 9 RHGP 13

## RESULT 27

Q8MH39 PRELIMINARY; PRT; 14 AA.  
AC Q8MH39;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "A new splicing acceptor site and polyadenylation sequence signal  
RT contribute to increase the extraordinary diversity of DQA1 mRNA  
RT isoforms."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' untranslated region."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF533901; AAM94815.1; -.  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1435 MW; C5E8A0FE15DF8EBD CRC64;  
Query Match  
Best Local Similarity 31.0%; Score 22; DB 7; Length 14;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 5 KHYGP 9  
: |||  
Db 9 RHQGP 13

## RESULT 28

Q8MH18 PRELIMINARY; PRT; 14 AA.  
AC Q8MH18;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "A new splicing acceptor site and polyadenylation sequence signal  
RT contribute to increase the extraordinary diversity of DQA1 mRNA  
RT isoforms."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' untranslated region."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF533922; AAM94836.1; -.  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1435 MW; C5E8A0FE15DF8EBD CRC64;  
Query Match  
Best Local Similarity 31.0%; Score 22; DB 7; Length 14;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

## RESULT 29

Q8MH55 PRELIMINARY; PRT; 14 AA.  
AC Q8MH55;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "HLA-DQA1 genes generate multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' UTR."  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF515808; AAM74915.1; -.  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1435 MW; C5E8A0FE15DF8EBD CRC64;  
Query Match  
Best Local Similarity 31.0%; Score 22; DB 7; Length 14;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 5 KHYGP 9  
: |||  
Db 9 RHQGP 13

## RESULT 30

Q8MH40 PRELIMINARY; PRT; 14 AA.  
AC Q8MH40;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "A new splicing acceptor site and polyadenylation sequence signal  
RT contribute to increase the extraordinary diversity of DQA1 mRNA  
RT isoforms."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' untranslated region."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF533900; AAM94814.1; -.  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1435 MW; C5E8A0FE15DF8EBD CRC64;  
Query Match  
Best Local Similarity 31.0%; Score 22; DB 7; Length 14;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9  
: |||  
Db 9 RHQGP 13

## RESULT 31

Q8MH07 PRELIMINARY; PRT; 14 AA.  
AC Q8MH07;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "A new splicing acceptor site and polyadenylation sequence signal  
RT contribute to increase the extraordinary diversity of DQA1 mRNA  
RT isoforms."  
RN Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' untranslated region."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF533933; AAM94847.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 14 AA; 1435 MW; C5EBA0FE15DF8EBD CRC64;  
Query Match  
Best Local Similarity 31.0%; Score 22; DB 7; Length 14;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 5 KHYGP 9  
: |||  
Db 9 RHQGP 13

## RESULT 32

Q8MH04 PRELIMINARY; PRT; 14 AA.  
AC Q8MH04;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "A new splicing acceptor site and polyadenylation sequence signal  
RT contribute to increase the extraordinary diversity of DQA1 mRNA  
RT isoforms."  
RN Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' untranslated region."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF533936; AAM94850.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 14 AA; 1435 MW; C5EBA0FE15DF8EBD CRC64;

Query Match  
Best Local Similarity 31.0%; Score 22; DB 7; Length 14;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9  
: |||  
Db 9 RHQGP 13

## RESULT 33

Q8MH52 PRELIMINARY; PRT; 14 AA.  
AC Q8MH52;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "HLA-DQA1 genes generate multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' UTR."  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF515811; AAM74918.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 14 AA; 1435 MW; C5EBA0FE15DF8EBD CRC64;

Query Match  
Best Local Similarity 31.0%; Score 22; DB 7; Length 14;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9  
: |||  
Db 9 RHQGP 13

## RESULT 34

Q8MH26 PRELIMINARY; PRT; 14 AA.  
AC Q8MH26;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "A new splicing acceptor site and polyadenylation sequence signal  
RT contribute to increase the extraordinary diversity of DQA1 mRNA  
RT isoforms."  
RN Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' untranslated region."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF533914; AAM94828.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 14 AA; 1435 MW; C5EBA0FE15DF8EBD CRC64;  
Query Match  
Best Local Similarity 31.0%; Score 22; DB 7; Length 14;

Best Local Similarity 60.0%; Pred. No. 5.5e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9  
: |||  
Db 9 RHQGP 13

## RESULT 35

Q8MH53 PRELIMINARY; PRT; 14 AA.  
AC Q8MH53;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "HLA-DQA1 gene generates multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' UTR."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF515810; AAM74917.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 14 AA; 1435 MW; CSEEA0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;  
Best Local Similarity 60.0%; Pred. No. 5.5e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9  
: |||  
Db 9 RHQGP 13

## RESULT 36

Q8MH20 PRELIMINARY; PRT; 14 AA.  
AC Q8MH20;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "A new splicing acceptor site and polyadenylation sequence signal  
RT contribute to increase the extraordinary diversity of DQA1 mRNA  
RT isoforms."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' untranslated region."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF533920; AAM94834.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 14 AA; 1435 MW; CSEEA0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;  
Best Local Similarity 60.0%; Pred. No. 5.5e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9  
: |||  
Db 9 RHQGP 13

## RESULT 37

Q8MH27 PRELIMINARY; PRT; 14 AA.  
AC Q8MH27;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "A new splicing acceptor site and polyadenylation sequence signal  
RT contribute to increase the extraordinary diversity of DQA1 mRNA  
RT isoforms."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' untranslated region."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF533913; AAM94827.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 14 AA; 1435 MW; CSEEA0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;  
Best Local Similarity 60.0%; Pred. No. 5.5e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9  
: |||  
Db 9 RHQGP 13

## RESULT 38

Q8MH05 PRELIMINARY; PRT; 14 AA.  
AC Q8MH05;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "A new splicing acceptor site and polyadenylation sequence signal  
RT contribute to increase the extraordinary diversity of DQA1 mRNA  
RT isoforms."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' untranslated region."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF533935; AAM94849.1; -.  
FT NON\_TER 1

Query Match 31.0%; Score 22; DB 7; Length 14;  
Best Local Similarity 60.0%; Pred. No. 5.5e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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SQ      SEQUENCE      14 AA;      1435 MW;      C5EEA0FE15DF8EBD CRC64;

Query Match                      31.0%;      Score 22;      DB 7;      Length 14;
Best Local Similarity          60.0%;      Pred. No. 5.5e+03;
Matches      3;      Conservative      1;      Mismatches      1;      Indels      0;      Gaps      0;

QY      5 KHYGP      9
      : |||
Db      9 RHQGP      13

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RESULT 39
Q8MH16
ID Q8MH16 PRELIMINARY; PRT; 14 AA.
AC Q8MH16;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533924; AAM94838.1; -.
FT NON TER 1 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;
Best Local Similarity 60.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 5 KHYGP 9
DB 9 RHQGP 13

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| RESULT | 40  |
|--------|---|
| OS     | 08MH38  |
| ID     | 08MH38  |
| AC     | 08MH38;   |
| DT     | 01-OCT-2002 (TReMBLrel. 22, Created)                              |
| DT     | 01-OCT-2002 (TReMBLrel. 22, Last sequence update)                 |
| DT     | 01-OCT-2002 (TReMBLrel. 22, Last annotation update)               |
| DE     | MHC class II antigen (Fragment).                                  |
| GN     | HLA-DQA1.   |
| OS     | Homo sapiens (Human).   |
| OC     | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC     | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.         |
| OX     | NCBI_Taxid=9606;  |
| RN     | [1]   |
| RP     | SEQUENCE FROM N.A.  |
| RA     | Hoarau J.-J., Cesari M., Cailiens H., Cadet F., Pabion M.;        |
| RT     | "A new splicing acceptor site and polyadenylation sequence signal |
| RT     | contribute to increase the extraordinary diversity of DQA1 mRNA   |
| RT     | isoforms.";   |
| RL     | Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.           |
| RN     | [2]   |
| RP     | SEQUENCE FROM N.A.  |
| RA     | Hoarau J.-J., Cesari M., Cailiens H., Cadet F., Pabion M.;        |

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RT      "HLA DQA1 gene generates multiple transcripts by alternative splicing
RT      and polyadenylation of the 3' untranslated region.";
RT      Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL      EMBL; AF533902; AAM94816.1; -.
DR      EMBL; AF533902; AAM94816.1; -.
FT      NON TER               1
SQ      SEQUENCE             14 AA;  1435 MW;  C5E8A0FE15DF8EBD CRC64;
Query Match             31.0%;   Score 22;   DB 7;   Length 14;
Best Local Similarity   60.0%;   Pred. No. 5.5e+03;
Matches      3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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|    |   |       |    |
|----|---|-------|----|
| QY | 5 | KHYCP | 9  |
|    | : |       |    |
| Db | 9 | RHOCP | 13 |

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RESULT 41
Q8MH56
ID Q8MH56 PRELIMINARY; PRT; 14 AA.
AC Q8MH56;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DOA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M.M., Caillens H., Cadet F., Pabion M.;
RT "HLA-DOA1 genes generate multiple transcripts by alternative splicing
RT and polyadenylation of the 3' UTR.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF515807; AAM74914.1; -.
FT NON TER 1 1
SQ SEQUENCE 14 AA; 1435 MW; CSEEA0FE15DF8EBD CRC64;

Query Match 31.0%; Score 22; DB 7; Length 14;
Best Local Similarity 60.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYGP 9
: |||
9 RHQGP 13
Db

```

```

RESULT 42
O8MH14
ID O8MH14 PRELIMINARY; PRT; 14 AA.
AC O8MH14;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Callens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQA1 mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Callens H., Cadet F., Pabion M.;
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region.";
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RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF533926; AAM94840.1; -  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1435 MW; C5EBA0FE15DF8EBD CRC64;  
Query Match  
Best Local Similarity 31.0%; Score 22; DB 7; Length 14;  
Matches 3; Conservativity 1; Mismatches 1; Indels 0; Gaps 0;  
QY 5 KHYGP 9  
Db 9 RHQGP 13  
RESULT 43  
Q8MH31 PRELIMINARY; PRT; 14 AA.  
AC Q8MH31;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "A new splicing acceptor site and polyadenylation sequence signal  
RT contribute to increase the extraordinary diversity of DQA1 mRNA  
RT isoforms."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "Hla DQA1 gene generates multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' untranslated region."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF533909; AAM94823.1; -  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1435 MW; C5EBA0FE15DF8EBD CRC64;  
Query Match  
Best Local Similarity 31.0%; Score 22; DB 7; Length 14;  
Matches 3; Conservativity 1; Mismatches 1; Indels 0; Gaps 0;  
QY 5 KHYGP 9  
Db 9 RHQGP 13  
RESULT 44  
Q8MH30 PRELIMINARY; PRT; 14 AA.  
AC Q8MH30;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "A new splicing acceptor site and polyadenylation sequence signal  
RT contribute to increase the extraordinary diversity of DQA1 mRNA  
RT isoforms."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

RN [2]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "Hla DQA1 gene generates multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' untranslated region."  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF533910; AAM94824.1; -  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1435 MW; C5EBA0FE15DF8EBD CRC64;  
Query Match  
Best Local Similarity 31.0%; Score 22; DB 7; Length 14;  
Matches 3; Conservativity 1; Mismatches 1; Indels 0; Gaps 0;  
QY 5 KHYGP 9  
Db 9 RHQGP 13  
RESULT 45  
Q8MH51 PRELIMINARY; PRT; 14 AA.  
AC Q8MH51;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE MHC class II antigen (Fragment).  
GN HLA-DQA1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;  
RT "Hla-DQA1 genes generate multiple transcripts by alternative splicing  
RT and polyadenylation of the 3' UTR."  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF515812; AAM74919.1; -  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1435 MW; C5EBA0FE15DF8EBD CRC64;  
Query Match  
Best Local Similarity 31.0%; Score 22; DB 7; Length 14;  
Matches 3; Conservativity 1; Mismatches 1; Indels 0; Gaps 0;  
QY 5 KHYGP 9  
Db 9 RHQGP 13

Search completed: August 30, 2004, 10:55:21  
Job time : 13.5912 secs



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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:09 ; Search time 1.89527 Seconds  
(without alignments)  
302.211 Million cell updates/sec

Title: US-09-720-469A-5  
Perfect score: 71  
Sequence: 1 NFKLKHYPGW 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues  
Total number of hits satisfying chosen parameters: 585

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID          | Description         |
|------------|-------|-------------|--------|----|-------------|---------------------|
| 1          | 29    | 40.8        | 11     | 1  | CA31_LITCI  | P82089 litoria cit  |
| 2          | 29    | 40.8        | 11     | 1  | CA32_LITCI  | P82090 litoria cit  |
| 3          | 28    | 39.4        | 8      | 1  | RPCH_PANBO  | P08939 pandalus bo  |
| 4          | 28    | 39.4        | 10     | 1  | HTF_NAUCI   | P10939 nauphoeta c  |
| 5          | 26    | 36.6        | 10     | 1  | GON2_CHICK  | P37043 gallus gall  |
| 6          | 26    | 36.6        | 10     | 1  | GONL_SQUTAC | P27429 squallus aca |
| 7          | 25    | 35.2        | 8      | 1  | AKH_MEML    | P25423 melolontha   |
| 8          | 25    | 35.2        | 8      | 1  | AKH_TABAT   | P14595 tabanus atr  |
| 9          | 25    | 35.2        | 10     | 1  | GON3_ONCKE  | P20367 oncorhynch   |
| 10         | 25    | 35.2        | 10     | 1  | HTF_TABAT   | P14596 tabanus atr  |
| 11         | 24    | 33.8        | 10     | 1  | BRK_ONCMY   | P09221 oncorhynch   |
| 12         | 23    | 32.4        | 10     | 1  | COXO_RAT    | P80432 rattus norv  |
| 13         | 23    | 32.4        | 10     | 1  | COXO_THUOB  | P80982 thunnus obe  |
| 14         | 22    | 31.0        | 8      | 1  | HTF1_PERAM  | P04548 periplaneta  |
| 15         | 22    | 31.0        | 8      | 1  | HTF_TENNO   | P25419 tenebrio mo  |
| 16         | 22    | 31.0        | 10     | 1  | GON1_PETMA  | P04378 petromyzon   |
| 17         | 22    | 31.0        | 11     | 1  | COR2_PERAM  | P11496 periplaneta  |
| 18         | 22    | 31.0        | 13     | 1  | BOML_PSEBU  | P42991 pseudophryn  |
| 19         | 20    | 28.2        | 8      | 1  | AKHG_GRYBI  | P14086 gryllus bim  |
| 20         | 20    | 28.2        | 8      | 1  | AKH_LIBAU   | P25418 libellula a  |
| 21         | 20    | 28.2        | 10     | 1  | HTF1_ROMMI  | P18110 romalea mic  |
| 22         | 20    | 28.2        | 12     | 1  | NUDM_CANPA  | P54713 canis fami   |
| 23         | 19.5  | 27.5        | 12     | 1  | RF1_CONSP   | P58805 conus spuri  |
| 24         | 19    | 26.8        | 8      | 1  | HTF2_PERAM  | P04549 periplaneta  |
| 25         | 19    | 26.8        | 10     | 1  | GON3_PETMA  | P30948 petromyzon   |
| 26         | 19    | 26.8        | 10     | 1  | HTF2_CARMO  | P11385 carausius m  |
| 27         | 19    | 26.8        | 10     | 1  | HTF_HELZE   | P16353 heliothis z  |
| 28         | 18    | 25.4        | 11     | 1  | CS15_BACSU  | P81095 bacillus su  |
| 29         | 18    | 25.4        | 13     | 1  | MLA_CAMDR   | P01198 camelus dro  |
| 30         | 18    | 25.4        | 13     | 1  | SA2A_ONCMY  | P82238 oncorhynch   |
| 31         | 18    | 25.4        | 13     | 1  | SA2B_ONCMY  | P82239 oncorhynch   |
| 32         | 18    | 25.4        | 13     | 1  | UN12_CLODA  | P81353 clostridium  |
| 33         | 18    | 25.4        | 14     | 1  | LPW_ECOLI   | P03053 escherichia  |

|    |    |      |    |   |            |                    |
|----|----|------|----|---|------------|--------------------|
| 34 | 18 | 25.4 | 14 | 1 | MCRZ_METTM | P58816 methanobact |
| 35 | 17 | 23.9 | 8  | 1 | ALL1_CYPBO | P82152 cydia pomon |
| 36 | 17 | 23.9 | 8  | 1 | CCKN_VACEU | P30369 macropus eu |
| 37 | 17 | 23.9 | 8  | 1 | UF06_MOUSE | P38644 mus musculu |
| 38 | 17 | 23.9 | 9  | 1 | LMIP_LOGMI | P31799 locusta mig |
| 39 | 17 | 23.9 | 10 | 1 | BPP_VIPAS  | P31351 vipera aspi |
| 40 | 17 | 23.9 | 10 | 1 | CA12_LITCI | P82086 litoria cit |
| 41 | 17 | 23.9 | 10 | 1 | CAER_LITXA | P56264 litoria xan |
| 42 | 17 | 23.9 | 10 | 1 | TKN1_SCYCA | P08608 scyllorhinu |
| 43 | 17 | 23.9 | 10 | 1 | TKS1_AEDAE | P42634 aedes aegyp |
| 44 | 17 | 23.9 | 10 | 1 | TKS2_AEDAE | P42635 aedes aegyp |
| 45 | 17 | 23.9 | 10 | 1 | UXA6_CHLTR | P38007 chlamydia t |

ALIGNMENTS

|                       |   |           |      |        |
|-----------------------|---|-----------|------|--------|
| RESULT 1              | CA31_LITCI  | STANDARD; | PRT; | 11 AA. |
| ID                    | CA31_LITCI  |           |      |        |
| AC                    | P82089;   |           |      |        |
| DT                    | 16-OCT-2001 (Rel. 40, Created)  |           |      |        |
| DT                    | 16-OCT-2001 (Rel. 40, Last sequence update)   |           |      |        |
| DT                    | 10-OCT-2003 (Rel. 42, Last annotation update)   |           |      |        |
| DE                    | Caerulein 3.1/3.1Y4.  |           |      |        |
| OS                    | Litoria citropa (Australian blue mountains tree frog).  |           |      |        |
| OC                    | Eukaryota; Metazoa; Chordata; Vertebrata; Euleleostomi;   |           |      |        |
| OC                    | Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;   |           |      |        |
| OC                    | Pelodyadinae; Litoria.  |           |      |        |
| OX                    | NCBI_TaxID=94770;   |           |      |        |
| RN                    | [1]   |           |      |        |
| RP                    | SEQUENCE, AND MASS SPECTROMETRY.  |           |      |        |
| RC                    | TISSUE=Skin secretion;  |           |      |        |
| RX                    | MEDLINE=20057701; PubMed=10589099;  |           |      |        |
| RA                    | Wabnitz P.A., Bowie J.H., Tyler M.J.;   |           |      |        |
| RT                    | "Caerulein-like peptides from the skin glands of the Australian blue mountains tree frog Litoria citropa. Part 1. Sequence determination using electrospray mass spectrometry." |           |      |        |
| RT                    | Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  |           |      |        |
| CC                    | - FUNCTION: Hypotensive neuropeptide (Probable).  |           |      |        |
| CC                    | - SUBCELLULAR LOCATION: Secreted.   |           |      |        |
| CC                    | - TISSUE SPECIFICITY: Skin dorsal glands.   |           |      |        |
| CC                    | - PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being sulfated.  |           |      |        |
| CC                    | - MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.  |           |      |        |
| CC                    | - SIMILARITY: Belongs to the gastrin/cholecystokinin family.  |           |      |        |
| DR                    | InterPro: IPR001651; Gastrin.   |           |      |        |
| DR                    | PROSITE: PS00259; GASTRIN; FALSE_NEG.   |           |      |        |
| KW                    | Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;   |           |      |        |
| KW                    | Pyroglutamate carboxylic acid.  |           |      |        |
| FT                    | MOD_RES 1   |           |      |        |
| FT                    | MOD_RES 4   |           |      |        |
| FT                    | MOD_RES 11  |           |      |        |
| FT                    | MOD_RES 1347  |           |      |        |
| FT                    | SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;  |           |      |        |
| QY                    | 7 YGPGW 11  |           |      |        |
| Db                    | 4 YGTGW 8   |           |      |        |
| Query Match           | 40.8%; Score 29; DB 1; Length 11;   |           |      |        |
| Best Local Similarity | 80.0%; Pred. No. 34;  |           |      |        |
| Matches               | 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  |           |      |        |
| RESULT 2              | CA32_LITCI  | STANDARD; | PRT; | 11 AA. |
| ID                    | CA32_LITCI  |           |      |        |
| AC                    | P82090;   |           |      |        |
| DT                    | 16-OCT-2001 (Rel. 40, Created)  |           |      |        |
| DT                    | 16-OCT-2001 (Rel. 40, Last sequence update)   |           |      |        |
| DT                    | 10-OCT-2003 (Rel. 42, Last annotation update)   |           |      |        |
| DE                    | Caerulein 3.2/3.2Y4.  |           |      |        |
| OS                    | Litoria citropa (Australian blue mountains tree frog).  |           |      |        |

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
OX Pelodyadinae; Litoria.  
NCBI\_TaxID=94770;  
RN [1]  
RP SEQUENCE AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RX MEDLINE=20057701; PubMed=10589099;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
RT "Caerulein-like peptides from the skin glands of the Australian blue  
RT mountains tree frog Litoria citropa. Part 1. Sequence determination  
RT using electrospray mass spectrometry.";  
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
CC -1- FUNCTION: Hypotensive neuropeptide (Probable).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin dorsal glands.  
CC -1- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being  
CC sulfated.  
CC -1- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.  
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR InterPro: IPR001651; Gastrin.  
DR PROSITE: PS00259; GASTRIN; FALSE NEG.  
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 4 4 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;  
  
Query Match 40.8%; Score 29; DB 1; Length 11;  
Best Local Similarity 80.0%; Pred. No. 34;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
OY 7 YGPGW 11  
DB 4 YGTGW 8  
  
RESULT 3  
RPCH\_PANBO STANDARD; PRT; 8 AA.  
ID RPCH\_PANBO  
AC P08939;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Red pigment concentrating hormone (RPCH).  
OS Pandanus borealis (Northern red shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandalioidea;  
OC Pandalidae; Pandalus.  
OX NCBI\_TaxID=6703;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75054965; PubMed=4433569;  
RA Fernlund P.;  
RT "Structure of the red-pigment-concentrating hormone of the shrimp,  
RT Pandanus borealis.";  
RL Biochim. Biophys. Acta 371:304-311(1974).  
CC -1- FUNCTION: This hormone adapts the animal to light backgrounds by  
CC stimulating concentration of the pigment of its red body-  
CC chromatophores.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.  
DR PIR; A61348; A61348.  
DR InterPro: IPR002047; AKH.  
DR PROSITE: PS00256; AKH; 1.  
KW Pigment; Hormone; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 948 MW; 86786775B9C44736 CRC64;  
  
Query Match 39.4%; Score 28; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
OY 6 HYGPW 11  
DB 3 NFSPGW 8  
  
RESULT 4  
HTF\_NAUCI STANDARD; PRT; 10 AA.  
ID HTF\_NAUCI  
AC P10939;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypertrehalosaemic hormone (HTH) (Hypertrehalosaemic neuropeptide).  
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),  
OS Leucophaea maderae (Madeira cockroach),  
OS Blattella germanica (German cockroach), and  
OS Gromphadorina portentosa (Madagascan hissing cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Nauphoeta.  
OX NCBI\_TaxID=6990, 6988, 6973, 36953;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=N.cinerea; TISSUE=Corpora cardiaca;  
RX MEDLINE=87100208; PubMed=3801028;  
RA Gaede G., Rinehart K.L. Jr.;  
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from  
RT the corpora cardiaca of the cockroaches Leucophaea maderae,  
RT Gromphadorina portentosa, Blattella germanica and Blatta orientalis  
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast  
RT atom bombardment mass spectrometry.";  
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=L.maderae, G.portentosa, and B.germanica;  
RX MEDLINE=91179584; PubMed=2080017;  
RA Veenstra J.A., Camps F.;  
RT "Structure of the hypertrehalosaemic neuropeptide of the German  
RT cockroach, Blattella germanica.";  
RL Neuropeptides 15:107-109(1990).  
CC -1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that  
CC elevate the level of trehalose in the hemolymph of insects).  
CC major carbohydrate in the hemolymph of insects).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.  
DR PIR; A26381; A26381.  
DR PIR; A60421; A60421.  
DR PIR; S08997; S08997.  
DR PIR; S08998; S08998.  
DR InterPro: IPR002047; AKH.  
DR PROSITE: PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1092 MW; 056236786775B9C4 CRC64;  
  
Query Match 39.4%; Score 28; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 47;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
OY 6 HYGPW 11  
DB 3 NFSPGW 8

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RESULT 5
GON2_CHICK STANDARD; PRT; 10 AA.
ID GON2_CHICK STANDARD; PRT; 10 AA.
AC P37043; P20408; P81750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin II (Gonadotropin-releasing hormone II) (GNRH-II)
DE (LH-RH II) (Luliberin II).
OS Gallus gallus (Chicken).
OS Alligator mississippiensis (American alligator),
OS Squalus acanthias (Spiny dogfish),
OS Hydrolagus colliei (Spotted ratfish) (Pacific ratfish), and
OS Clupea pallasii (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031, 8496, 7797, 7873, 30724;
RN [1]
RP SEQUENCE.
RC SPECIES=Chicken; TISSUE=Hypothalamus;
RX MEDLINE=84222059; PubMed=6427779;
RA Miyamoto K., Hasegawa Y., Nomura M., Igarashi M., Kangawa K.,
RA Matsuo H.;
RT "Identification of the second gonadotropin-releasing hormone in
RT chicken hypothalamus: evidence that gonadotropin secretion is
RT probably controlled by two distinct gonadotropin-releasing hormones
RT in avian species.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3874-3878(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=A.mississippiensis; TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McGory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
RN [3]
RP SEQUENCE.
RC SPECIES=S.acanthias; TISSUE=Brain;
RX MEDLINE=92335300; PubMed=1631133;
RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
RA Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) in
RT dogfish brain provides insight into GNRH evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).
RN [4]
RP SEQUENCE.
RC SPECIES=H.colliei; TISSUE=Brain;
RX MEDLINE=91340067; PubMed=1678723;
RA Lovejoy D.A., Sherwood N.M., Fischer W.H., Jackson B.C., Rivier J.E.,
RA Lee T.;
RT "Primary structure of gonadotropin-releasing hormone from the brain
RT of a holoccephalan (ratfish, Hydrolagus colliei).";
RL Gen. Comp. Endocrinol. 82:152-161(1991).
RN [5]
RP SEQUENCE, AND FUNCTION.
RC SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
RX MEDLINE=20114351; PubMed=10650929;
RA Carolisfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
RT hormones, including a novel form, from an ancient teleost, herring.";
RL Endocrinology 141:505-512(2000).
CC -1- FUNCTION: Stimulates the secretion of gonadotropins.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the GNRH family.
DR PIR; A61126; A61126.
DR PIR; B46030; B46030.
DR PIR; B60066; RHA02.

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DR InterPro; IPR002012; GNRH.
DR Pfam; PF00446; GNRH; 1.
DR PROSITE; PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1254 MW; 284B2E437871F5A3 CRC64;

Query Match 36.6%; Score 26; DB 1; Length 10;
Best Local Similarity 42.9%; Pred. No. 1e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 KHYPGW 11
Db 1 QHWSHG 7

RESULT 6
GONL_SQUAC STANDARD; PRT; 10 AA.
ID GONL_SQUAC STANDARD; PRT; 10 AA.
AC P27429;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin (Gonadotropin-releasing hormone) (GNRH) (LH-RH)
DE (Luliberin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92335300; PubMed=1631133;
RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
RA Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) in
RT dogfish brain provides insight into GNRH evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).
CC -1- FUNCTION: Stimulates the secretion of gonadotropins.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the GNRH family.
DR PIR; A46030; A46030.
DR InterPro; IPR002012; GNRH.
DR Pfam; PF00446; GNRH; 1.
DR PROSITE; PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;

Query Match 36.6%; Score 26; DB 1; Length 10;
Best Local Similarity 42.9%; Pred. No. 1e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 KHYPGW 11
Db 1 QHWSHG 7

RESULT 7
AKH_MEIHL STANDARD; PRT; 8 AA.
ID AKH_MEIHL STANDARD; PRT; 8 AA.
AC P25423;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokine hormone (AKH).
OS Melolontha melolontha (Cockchafer),
OS Geotrupes stercorarius (Dor beetle), and
OS Pachnoda marginata (Flower beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;

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OC Scarabaeidae; Melolonthinae; Melolontha.  
OX NCBI\_TaxID=7061, 7087, 7058;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=M.melolontha, and G.stercorarius; TISSUE=Corpora cardiaca;  
RX MEDLINE=91248100; PubMed=2039445;  
RA Gaede G.;  
RT "A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone peptide family isolated and sequenced from two beetle species."  
RT Biochem. J. 275:671-677(1991).  
RN [2]  
RN SEQUENCE.  
RC SPECIES=P.marginata; TISSUE=Corpora cardiaca;  
RX MEDLINE=92265187; PubMed=1586453;  
RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;  
RT "Primary structures of neuropeptides isolated from the corpora cardiaca of various cetoniid beetle species determined by pulsed-liquid phase sequencing and tandem fast atom bombardment mass spectrometry."  
RT Biol. Chem. Hoppe-Seyler 373:133-142(1992).  
CC -!- FUNCTION: This hormone, released from cells in the corpora cardiaca after the beginning of flight, causes release of diglycerides from the fat body and then stimulates the flight muscles to use these diglycerides as an energy source.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.  
DR PIR; A58641; A58641.  
DR PIR; S15422; S15422.  
DR PIR; S21663; S21663.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;  
  
Query Match 35.2%; Score 25; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6 HYGPGW 11  
Db 3 NYSPDW 8  
  
RESULT 8  
AKH\_TABAT STANDARD; PRT; 8 AA.  
ID AKH\_TABAT  
AC P14595;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I) (DCC I).  
OS Tabanus atratus (Horse fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae; Tabanus.  
OC NCBI\_TaxID=7207;  
RN [1]  
RN SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=90046758; PubMed=2813385;  
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J., Vogel V.W., Zhang Y.S., Hayes D.K.;  
RT "Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activity isolated from the corpora cardiaca of horse flies (Diptera)."  
RT Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).  
CC -!- FUNCTION: This hormone, released from cells in the corpora cardiaca after the beginning of flight, causes release of diglycerides from the fat body and then stimulates the flight

CC muscles to use these diglycerides as an energy source.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.  
DR PIR; A33995; A33995.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;  
  
Query Match 35.2%; Score 25; DB 1; Length 8;  
Best Local Similarity 60.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 YGPGW 11  
Db 4 FTPGW 8  
  
RESULT 9  
GON3\_ONCKE STANDARD; PRT; 10 AA.  
ID GON3\_ONCKE  
AC P20367; P81751;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GnRH-III) (LH-RH III) (Luliberin III).  
DE RH III (Luliberin III).  
GN GNRH3.  
OS Oncorhynchus keta (Chum salmon), and  
OS Clupea pallasii (Pacific herring).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8018, 30724;  
RN [1]  
RN SEQUENCE.  
RC SPECIES=O.keta;  
RX MEDLINE=83195140; PubMed=6341999;  
RA Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;  
RT "Characterization of a teleost gonadotropin-releasing hormone."  
RT Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).  
RN [2]  
RN SEQUENCE, AND FUNCTION.  
RC SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;  
RX MEDLINE=20114351; PubMed=10650929;  
RA Carolstfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G., Chang J.P., Rivier J.E., Sherwood N.M.;  
RT "Primary structure and function of three gonadotropin-releasing hormones, including a novel form; from an ancient teleost, herring."  
RT Endocrinology 141:505-512(2000).  
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the GNRH family.  
DR PIR; A21114; A21114.  
DR InterPro; IPR002012; GNRH.  
DR Pfam; PF00446; GNRH; 1.  
DR PROSITE; PS00473; GNRH; 1.  
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;  
  
Query Match 35.2%; Score 25; DB 1; Length 10;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 5 KHYPGW 11  
Db 1 QHWSYGW 7

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RESULT 10
HTF_TABAT
ID HTF_TABAT STANDARD; PRT; 10 AA.
AC P14596;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor (HOTH) (Dipteran corpora cardiaca factor II)
DE (DCC II).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neurotrophic hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -1- FUNCTION: Hypertrehalosaemic factors are neurotrophic that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPNH family.
DR PIR; B33995; B33995.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KM Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;

Query Match 35.2%; Score 25; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGW 11
: |||
Db 4 FTPGW 8

RESULT 11
BRK_ONCMY STANDARD; PRT; 10 AA..
ID BRK_ONCMY
AC Q9PRZ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysyl-bradykinin-like.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
RT trout plasma.";
RL FEBS Lett. 334:75-78(1993).
CC -1- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR
CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- SIMILARITY: Belongs to the bradykinin family.

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DR PIR; S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 33.8%; Score 24; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGW 11
: |||
Db 4 PGW 6

RESULT 12
COXO_RAT STANDARD; PRT; 10 AA.
ID COXO_RAT
AC P80432;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIC, mitochondrial (EC 1.9.3.1)
DE (VIIC) (Fragment).
GN COX7C OR COX7C1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform.";
RL Eur. J. Biochem. 230:235-241(1995).
CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.
DR PIR; S65388; S65388.
KM Oxidoreductase; Mitochondrion.
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1117 MW; 126DE767687B1B0B CRC64;

Query Match 32.4%; Score 23; DB 1; Length 10;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 6 HY--GPG 10
: |||
Db 2 HYEGLPG 8

RESULT 13
COXO_THUOB STANDARD; PRT; 10 AA.
ID COXO_THUOB
AC P80982;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;

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RX MEDLINE=97454291; PubMed=9310366;  
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,  
RA Kadenbach B.;  
RT "The subunit structure of cytochrome-c oxidase from tuna heart and  
RT liver";  
RL Eur. J. Biochem. 248:99-103(1997).  
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide  
CC chains of cytochrome c oxidase, the terminal oxidase in  
CC mitochondrial electron transport.  
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.  
DR PIR; S77990; S77990.  
KW Oxidoreductase; inner membrane; Mitochondrion.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1059 MW; 126DE767687B1DCB CRC64;  
  
Query Match 32.4%; Score 23; DB 1; Length 10;  
Best Local Similarity 71.4%; Pred. No. 3.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;  
  
QY 6 HY--GPG 10  
DB 2 HYAEGPG 8  
  
RESULT 14  
HTF1\_PERAM STANDARD; PRT; 8 AA.  
ID HTF1\_PERAM  
AC P04548;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypertrehalosaemic factor I (Neuropeptide M-I) (Periplanetin CC-I)  
DE (Pea-CAH-I) (LSD-CC-I) (Hypertrehalosaemic neuropeptide I).  
OS Periplaneta americana (American cockroach).  
OS Lepidoptera decemlineata (Colorado potato beetle), and  
OS Blatta orientalis (Oriental cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978, 7539, 6976;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=P.americana;  
RX MEDLINE=85046530; PubMed=6548628;  
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,  
RA Rinehart K.L. Jr.;  
RT "Structures of two cockroach neuropeptides assigned by fast atom  
RT bombardment mass spectrometry";  
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=P.americana;  
RX MEDLINE=84298179; PubMed=6591205;  
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,  
RA Miller C.A., Schooley D.A.;  
RT "Isolation and primary structure of two peptides with  
RT cardioacceleratory and hyperglycemic activity from the corpora  
RT cardiaca of Periplaneta americana";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;  
RX MEDLINE=90160053; PubMed=2576128;  
RA Gaede G., Keilner R.;  
RT "The metabolic neuropeptides of the corpus cardiacum from the potato  
RT beetle and the American cockroach are identical.";  
RL Peptides 10:1287-1289(1989).  
RN [4]  
RP SEQUENCE.  
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;

RX MEDLINE=90253659; PubMed=2340112;  
RA Gaede G., Rinehart K.L. Jr.;  
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from  
RT the corpora cardiaca of the cockroaches Leucophaea maderae,  
RT Gromphodrhina portentosa, Blatteia germanica and Blatta orientalis  
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast  
RT atom bombardment mass spectrometry";  
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that  
CC elevate the level of trehalose in the hemolymph (trehalose is  
CC the major carbohydrate in the hemolymph of insects).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.  
DR PIR; A05169; A05169.  
DR PIR; A44960; A44960.  
DR PIR; A49823; A49823.  
DR PIR; S08995; S08995.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1  
FT MOD\_RES 8 8  
SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;  
  
Query Match 31.0%; Score 22; DB 1; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6 HYPGW 11  
DB 3 NFSPNW 8  
  
RESULT 15  
HTF\_TENMO STANDARD; PRT; 8 AA.  
ID HTF\_TENMO  
AC P25419;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypertrehalosaemic factor (HOTH) (Hypertrehalosemic neuropeptide).  
OS Tenebrio molitor (Yellow mealworm), and  
OS Zophobas rugipes.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
OC Tenebrionidae; Tenebrio.  
OX NCBI\_TaxID=7067, 7075;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=T.molitor, and Z.rugipes;  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=90341081; PubMed=2381871;  
RA Gaede G., Rosinski G.;  
RT "The primary structure of the hypertrehalosemic neuropeptide from  
RT tenebrionid beetles: a novel member of the AKH/RPCH family.";  
RL Peptides 11:455-459(1990).  
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that  
CC elevate the level of trehalose in the hemolymph (trehalose is the  
CC major carbohydrate in the hemolymph of insects).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.  
DR PIR; A43976; A43976.  
DR PIR; B43976; B43976.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1  
FT MOD\_RES 8 8  
SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;  
  
Query Match 31.0%; Score 22; DB 1; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;



QY 6 HYGPGW 11  
 Db 3 NFSPNW 8

RESULT 16  
 GONI\_PETMA STANDARD; PRT; 10 AA.  
 AC P04378;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 20-MAR-1987 (Rel. 04, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I)  
 DE (Luliberin I).  
 OS Petromyzon marinus (Sea lamprey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.  
 OX NCBI\_TaxID=7757;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=86168192; PubMed=3514603;  
 RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.U.;  
 RT "Primary structure of gonadotropin-releasing hormone from lamprey  
 brain.";  
 RL J. Biol. Chem. 261:4812-4819(1986).  
 CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates  
 the secretion of both luteinizing and follicle-stimulating  
 hormones.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the GnRH family.  
 DR PIR; A01412; RHLMS.  
 DR InterPro; IPR002012; GnRH.  
 DR Pfam; PF00446; GnRH; 1.  
 DR PROSITE; PS00473; GnRH; 1.  
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1244 MW; 1E4B36237B1735AB CRC64;

Query Match 31.0%; Score 22; DB 1; Length 10;  
 Best Local Similarity 42.9%; Pred. No. 5.2e+02;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KHYGPGW 11  
 Db 1 QHYSLEW 7

RESULT 17  
 CORZ\_PERAM STANDARD; PRT; 11 AA.  
 ID CORZ\_PERAM  
 AC P1436;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Corazonin.  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=89325572; PubMed=2753132;  
 RA Veenstra J.A.;  
 RT "Isolation and structure of corazonin, a cardioactive peptide from  
 the American cockroach.";  
 RL FEBS Lett. 250:231-234(1989).  
 CC -1- FUNCTION: Cardioactive peptide. Corazonin is probably involved  
 in the physiological regulation of the heart beat.

CC -1- SUBCELLULAR LOCATION: Secreted.  
 DR PIR; S05002; S05002.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 31.0%; Score 22; DB 1; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 5.7e+02;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 YGPGW 11  
 Db 5 YSRGW 9

RESULT 18  
 BOML\_PSEGU STANDARD; PRT; 13 AA.  
 ID BOML\_PSEGU  
 AC P42951;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Bombesin-like peptide L (PG-L).  
 OS Pseudophryne guntheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 the Australian frog Pseudophryne guntheri.";  
 RL Peptides 11:299-304(1990).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin  
 family.  
 DR PIR; A60409; A60409.  
 DR InterPro; IPR000874; Bombesin.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Amphibian defense peptide; Bombesin family; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 13 13 AMIDATION.  
 SQ SEQUENCE 13 AA; 1372 MW; D6DE0D24BD98C366 CRC64;

Query Match 31.0%; Score 22; DB 1; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 6.8e+02;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 GPGW 11  
 Db 4 GPQW 7

RESULT 19  
 AKHG\_GRYBI STANDARD; PRT; 8 AA.  
 ID AKHG\_GRYBI  
 AC P14086;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Adipokine hormone G (AKH-G) (RO II).  
 OS Gryllus bimaculatus (Two-spotted cricket), and  
 OS Romalea microptera (Lubber grasshopper).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;

OC Gryllus.  
OX NCB1\_TaxID=6999, 7007;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;  
RX MEDLINE=8106553; PubMed=3426616;  
RA Gaede G., Rinehart K.L. Jr.;  
RT "Primary sequence analysis by fast atom bombardment mass spectrometry of a peptide with adipokinetic activity from the corpora cardiaca of the cricket Gryllus bimaculatus.";  
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;  
RX MEDLINE=89145002; PubMed=3226948;  
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;  
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from the lubber grasshopper, Romalea microptera.";  
RL Peptides 9:681-688(1988).  
CC -!- FUNCTION: This hormone, released from cells in the corpora cardiaca after the beginning of flight, causes release of diglycerides from the fat body and then stimulates the flight muscles to use these diglycerides as an energy source.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.  
DR PIR; A28004; A28004.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 8 AMIDATION.  
FT MOD\_RES 1 8 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;  
  
Query Match 28.2%; Score 20; DB 1; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6 HYGPGW 11  
Db 3 NFTPSTW 8  
  
RESULT 20  
AKH\_LIBAU STANDARD; PRT; 8 AA.  
ID AKH\_LIBAU  
AC P25418;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Adipokinetic hormone (AKH).  
OS Libellula auripennis (Skimmer dragonfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.  
OX NCB1\_TaxID=6966;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=90359055; PubMed=2390213;  
RA Gaede G.;  
RT "The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hormone family isolated and sequenced from a dragonfly.";  
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).  
CC -!- FUNCTION: This hormone, released from cells in the corpora cardiaca after the beginning of flight, causes release of diglycerides from the fat body and then stimulates the flight muscles to use these diglycerides as an energy source.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.  
DR PIR; S10596; S10596.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;  
  
Query Match 28.2%; Score 20; DB 1; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6 HYGPGW 11  
Db 3 NFTPSTW 8  
  
RESULT 21  
HTF1\_ROMMI STANDARD; PRT; 10 AA.  
ID HTF1\_ROMMI  
AC P18110;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE RO I (Hypertrehalosaemic factor).  
OS Romalea microptera (lubber grasshopper).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha; OC Acridoidea; Romaleidae; Romalea.  
OX NCB1\_TaxID=7007;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=89145002; PubMed=3226948;  
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;  
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from the lubber grasshopper, Romalea microptera.";  
RL Peptides 9:681-688(1988).  
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that elevate the level of trehalose in the hemolymph of insects).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;  
  
Query Match 28.2%; Score 20; DB 1; Length 10;  
Best Local Similarity 33.3%; Pred. No. 1.2e+03;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6 HYGPGW 11  
Db 3 NFTPSTW 8  
  
RESULT 22  
NUDM\_CANFA STANDARD; PRT; 12 AA.  
ID NUDM\_CANFA  
AC P54713;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE NADH-ubiquinone oxidoreductase 42 kDa subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-42KD) (CI-42KD) (Fragment).  
OS NUDFAL0.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCB1\_TaxID=9615;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Heart;  
RX MEDLINE=98163340; PubMed=9504812;



RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
RT dog heart proteins.";  
RL Electrophoresis 18:2795-2802(1997).  
CC -1- FUNCTION: Transfer of electrons from NADH to the respiratory  
CC chain. The immediate electron acceptor for the enzyme is believed  
CC to be ubiquinone.  
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
CC -1- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.  
CC -1- COFACTOR: Binds 1 FAD per subunit.  
CC -1- SUBUNIT: Mammalian complex I is composed of 45 different subunits.  
CC This a component of the hydrophobic protein fraction.  
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
DR HSC-2DPAGE; P54713; DOG.  
KM Oxidoreductase; NAD; Ubiquinone; Flavoprotein; FAD; Mitochondrion.  
FT NON TER 12 12  
SQ SEQUENCE 12 AA; 1284 MW; 3CCDAE2B36EDD737 CRC64;  
  
Query Match 28.2%; Score 20; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 YGP 9  
Db 3 YGP 5  
  
RESULT 23  
RF1\_CONSP  
ID RF1\_CONSP STANDARD; PRT; 12 AA.  
AC P58805;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Conorfamide-Sti.  
OS Conus spurius (Alphabet cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_Taxid=192919;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=21605839; PubMed=11738233;  
RA Maillo M., Aguilar M.B., Lopez-Vera E., Craig A.G., Bulaj G.,  
RA Olivera B.M., Heimer de la Cotera E.P.;  
RT "Conorfamide, a Conus venom peptide belonging to the Rfamide family of  
RT neuropeptides.";  
RT Toxicol 40:401-407(2002).  
RL -1- FUNCTION: Causes hyperactivity in mice.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -1- MASS SPECTROMETRY: MW=1454.8; METHOD=Electrospray.  
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
CC family.  
KM Neurotoxin; Toxin; Amidation.  
FT MOD\_RES 12 12  
SQ SEQUENCE 12 AA; 1456 MW; 2510671E49D772D3 CRC64;  
  
Query Match 27.5%; Score 19.5; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1.7e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
  
QY 8 GP-GW 11  
Db 1 GPMGW 5  
  
RESULT 24  
HTF2\_PERAM  
ID HTF2\_PERAM STANDARD; PRT; 8 AA.  
AC P04549;  
DT 13-AUG-1987 (Rel. 05, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypertrehalosaemic factor II (Neuropeptide M-II) (Periplanetic CC-2)  
DE (Pea-CAH-II) (Led-CC-II) (Hypertrehalosaemic neuropeptide II).  
OS Periplaneta americana (American cockroach),  
OS Leptinotarsa decemlineata (Colorado potato beetle), and  
OS Blatta orientalis (Oriental cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_Taxid=6978, 7539, 6976;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=P.americana;  
RX MEDLINE=85046530; PubMed=6548628;  
RA Witten J.L., Schaffer M.H., O'Shea W., Cook J.C., Hemling M.E.,  
RA Rinehart K.L. Jr.;  
RT "Structures of two cockroach neuropeptides assigned by fast atom  
RT bombardment mass spectrometry.";  
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=P.americana;  
RX MEDLINE=84298179; PubMed=6591205;  
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,  
RA Miller C.A., Schooley D.A.;  
RT "Isolation and primary structure of two peptides with  
RT cardioacceleratory and hyperglycemic activity from the corpora  
RT cardiaca of Periplaneta americana.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;  
RX MEDLINE=90160053; PubMed=2576128;  
RA Gaede G., Kellner R.;  
RT "The metabolic neuropeptides of the corpus cardiaca from the potato  
RT beetle and the American cockroach are identical.";  
RL Peptides 10:1287-1289(1989).  
RN [4]  
RP SEQUENCE.  
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;  
RX MEDLINE=90253659; PubMed=2340112;  
RA Gaede G., Rinehart K.L. Jr.;  
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from  
RT the corpora cardiaca of the cockroaches Leucophaea maderae,  
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis  
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast  
RT atom bombardment mass spectrometry.";  
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
RL -1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that  
CC elevate the level of trehalose in the hemolymph (trehalose is the  
CC major carbohydrate in the hemolymph of insects).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.  
CC PIR; B44960; B44960.  
DR PIR; B49823; B49823.  
DR PIR; S08996; S08996.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KM Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1  
FT MOD\_RES 8 8  
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;  
  
Query Match 26.8%; Score 19; DB 1; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 7 YGPGW 11  
Db 4 FTPNW 8

RESULT 25  
GON3\_PETMA STANDARD; PRT; 10 AA.  
AC P30948;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GNRH-III)  
DE (Luliberin III).  
OS Petromyzon marinus (Sea lamprey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OC Petromyzontiformes; Petromyzontidae; Petromyzon.  
OX NCBI\_TaxID=7757;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=93178316; PubMed=8440174;  
RA Sower S.A., Chiang Y.-C., Iovas S., Conlon J.M.;  
RT "Primary structure and biological activity of a third gonadotropin-  
RT releasing hormone from lamprey brain.";  
RL Endocrinology 132:1125-1131(1993).  
CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates  
CC the secretion of both luteinizing and follicle-stimulating  
CC hormones.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the GNRH family.  
DR InterPro: IPR002012; GNRH.  
DR Pfam: PF00446; GNRH; 1.  
DR PROSITE: PS00473; GNRH; 1.  
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1277 MW; 284B36237AA1F5A3 CRC64;  
  
Query Match 26.8%; Score 19; DB 1; Length 10;  
Best Local Similarity 28.6%; Pred. No. 1.7e+03;  
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
QY 5 KHYPGW 11  
Db 1 QHMSHDW 7  
  
RESULT 26  
HTF2\_CARMO STANDARD; PRT; 10 AA.  
ID HTF2\_CARMO  
AC P11385;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypertrehalosaemic factor II (HTF-II) (HRTII) (Hypertrehalosaemic  
DE neuropeptide II).  
RN [1]  
OS Carausius morosus (Indian stick insect), and  
OS Extatosoma tiaratum (Stick insect).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatodea;  
OC Heteronemidae; Carausius.  
OX NCBI\_TaxID=7022, 7024;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;  
RX MEDLINE=87157103; PubMed=3828078;  
RA Gaede G., Rinehart K.L. Jr.;  
RT "Primary structure of the hypertrehalosaemic factor II from the  
RT corpus cardiaca of the Indian stick insect, Carausius morosus,  
RT determined by fast atom bombardment mass spectrometry.";  
RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;  
RX MEDLINE=90253659; PubMed=2340112;  
RA Gaede G., Rinehart K.L. Jr.;  
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from

RT the corpora cardiaca of the cockroaches Leucophaea maderae,  
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis  
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast  
RT atom bombardment mass spectrometry.";  
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
RN [3]  
RP CARBOHYDRATE-LINKAGE SITE.  
RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;  
RX MEDLINE=93129188; PubMed=1482345;  
RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;  
RT "A tryptophan-substituted member of the AKH/RPCH family isolated from  
RT a stick insect corpus cardiaca.";  
RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).  
CC -1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that  
CC elevate the level of trehalose in the hemolymph (trehalose is the  
CC major carbohydrate in the hemolymph of insects).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- MASS SPECTROMETRY: MW=1308.61; METHOD=FAB.  
CC -1- SIMILARITY: Belongs to the AKH / HRTII / RPCH family.  
DR PIR: JC1416; JC1416.  
DR PIR: S09138; S09138.  
DR InterPro: IPR002047; AKH.  
DR PROSITE: PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 C-LINKED (MAN) (PROBABLE).  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;  
  
Query Match 26.8%; Score 19; DB 1; Length 10;  
Best Local Similarity 40.0%; Pred. No. 1.7e+03;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 7 YGPGW 11  
Db 4 FTPNW 8  
  
RESULT 27  
HTF\_HELZE STANDARD; PRT; 10 AA.  
ID HTF\_HELZE  
AC P16353;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypertrehalosaemic hormone (Hez-HRTH).  
OS Heliothis zea (Corn earworm) (Bollworm).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Noctuidae; Heliothinae; Helicoverpa.  
OX NCBI\_TaxID=7113;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=88326324; PubMed=3415690;  
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,  
RA Tseng C.M., Zhang Y.S., Hayes D.K.;  
RT "Isolation and primary structure of a neuropeptide hormone from  
RT Heliothis zea with hypertrehalosemic and adipokinetic activities.";  
RL Biochem. Biophys. Res. Commun. 155:344-350(1988).  
CC -1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that  
CC elevate the level of trehalose in the hemolymph (trehalose is the  
CC major carbohydrate in the hemolymph of insects).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the AKH / HRTII / RPCH family.  
DR PIR: A31571; A31571.  
DR InterPro: IPR002047; AKH.  
DR PROSITE: PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;



RC TISSUE=Serum;  
RA Henry M.A., Secombes C.J.;  
RT "Purification and partial characterization of antibacterial peptides  
from rainbow trout, *Oncorhynchus mykiss*.";  
RL Submitted (DEC-1999) to Swiss-Prot.  
CC -!- FUNCTION: Antibacterial activity against Gram-negative bacteria.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Plasma serum.  
KW Antibiotic.  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1400 MW; 5FFB792AEABE5873 CRC64;  
  
Query Match  
Best Local Similarity 25.4%; Score 18; DB 1; Length 13;  
Matches 4; Conservativity 66.7%; Pred. No. 3.3e+03;  
Matches 4; Conservativity 0; Mismatches 2; Indels 0; Gaps 0;  
  
OY 2 FKLKHY 7  
DB 3 FVLKGY 8  
  
RESULT 32  
UN12\_CLOPA STANDARD; PRT; 13 AA.  
AC P81353;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Unknown protein CP 12 from 2D-page (Fragment).  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1501;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=WS;  
RX MEDLINE=98291870; PubMed=9629918;  
RA Flensburg R., Skjeldal L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal  
sequence analysis of proteins from Clostridium pasteurianum WS.";  
RL Electrophoresis 19:802-806(1998).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 5.8, ITS MW IS: 42.7 kDa.  
FT VARIANT 4 4 L -> V.  
FT VARIANT 5 5 Q -> I.  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1465 MW; 70AA9E98455D405B CRC64;  
  
Query Match  
Best Local Similarity 25.4%; Score 18; DB 1; Length 13;  
Matches 3; Conservativity 33.3%; Pred. No. 3.3e+03;  
Matches 3; Conservativity 2; Mismatches 4; Indels 0; Gaps 0;  
  
OY 2 FKLKHYGPG 10  
DB 2 YVLQGINPG 10  
  
RESULT 33  
LPM\_ECOLI STANDARD; PRT; 14 AA.  
AC P03053;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE TRP operon leader peptide.  
GN TRPL OR TRPE OR B1265 OR C5494 OR Z2545 OR ECS1837 OR SF1268 OR  
GN S4805.  
OS Escherichia coli,  
OS Escherichia coli O6,  
OS Escherichia coli O157:H7, and  
OS Shigella flexneri.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.

OX NCBI\_TaxID=562, 217992, 83334, 623;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=E.coli;  
RX MEDLINE=82150258; PubMed=7038627;  
RA Yanofsky C., Platt T., Crawford I.P., Nichols B.P., Christie G.E.,  
RA Horowitz H., van Cleemput M., Wu A.M.;  
RT "The complete nucleotide sequence of the tryptophan operon of  
RT Escherichia coli.";  
RL Nucleic Acids Res. 9:6647-6668(1981).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=E.coli;  
RX MEDLINE=76240562; PubMed=781271;  
RA Squires C., Lee F., Bertrand K., Squires C.L., Bronson M.J.,  
RA Yanofsky C.;  
RT "Nucleotide sequence of the 5' end of tryptophan messenger RNA of  
RT Escherichia coli.";  
RL J. Mol. Biol. 103:351-381(1976).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=E.coli;  
RX MEDLINE=80101455; PubMed=118451;  
RA Oxender D.L., Zurawski G., Yanofsky C.;  
RT "Attenuation in the Escherichia coli tryptophan operon: role of RNA  
RL secondary structure involving the tryptophan codon region.";  
RN [4]  
RP SEQUENCE FROM N.A.  
RC SPECIES=E.coli; STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;  
RX MEDLINE=22388234; PubMed=12471157;  
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,  
RA Rasko D., Buckles E.L., Lyon S.-R., Boutin A., Hackett J., Stroud D.,  
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;  
RT "Extensive mosaic structure revealed by the complete genome sequence  
RT of uropathogenic Escherichia coli.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;  
RX MEDLINE=21074935; PubMed=11206551;  
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
RA Welch R.A., Blattner F.R.;  
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";  
RL Nature 409:529-533(2001).  
RN [7]  
RP SEQUENCE FROM N.A.  
RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;  
RX MEDLINE=21156231; PubMed=11258796;  
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,  
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;  
RT "Complete genome sequence of enterohemorrhagic Escherichia coli  
RT O157:H7 and genomic comparison with a laboratory strain K-12.";  
RL DNA Res. 8:11-22(2001).  
RN [8]  
RP SEQUENCE FROM N.A.

```
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN (9)
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J01714; AAA57296.1; -.
DR EMBL; A04494; CAA00361.1; -.
DR EMBL; AE000224; AAC74347.1; -.
DR EMBL; AE016760; AAN80196.1; -.
DR EMBL; AE005380; AAG56550.1; -.
DR EMBL; AP002556; BAB35260.1; -.
DR EMBL; AB015153; AAN42881.1; -.
DR EMBL; AE016982; AAP16766.1; -.
DR PIR; A03589; LFECW.
DR PIR; B85761; B85761.
DR PIR; E90858; E90858.
DR EcoGene; EG1274; trpL.
KW Tryptophan biosynthesis; Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA; 1723 MW; 5B79306E3E804A37 CRC64;

Query Match 25.4%; Score 18; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.6e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

QY 2 FKLKHYGPGW 11
DB 5 FVLK----GW 10

RESULT 34
MCRZ_METTM STANDARD; PRT; 14 AA.
AC P58816;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Methyl-coenzyme M reductase II gamma subunit (EC 1.8.-.-) (MCR II
DE gamma) (Fragment).
GN MRTG.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
CX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=91099370; PubMed=2269306;
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RA Rospert S., Linder D., Ellermann J., Thauer R.K.;
RT "Two genetically distinct methyl-coenzyme M reductases in
RT Methanobacterium thermoautotrophicum strain Marburg and delta H.";
RL Eur. J. Biochem. 194:871-877(1990).
CC -!- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)
CC ethanesulfonic acid) with 7-mercaptoheptanoylthreosine phosphate
CC to methane and an heterodisulfide.
CC -!- CATALYTIC ACTIVITY: CH(3)-S-COM + H-S-HTP = CH(4) + COM-S-S-HTP.
CC -!- COFACTOR: Binds 2 coenzyme F430 noncovalently per hexamer.
CC Coenzyme F430 is a yellow nickel porphyrinoid.
CC -!- PATHWAY: Methanogenesis; last step.
CC -!- SUBUNIT: Hexamer of two alpha, two beta, and two gamma chains.
CC -!- DEVELOPMENTAL STAGE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA.
CC MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS
CC CONTAINS MOSTLY MCR I.
DR PIR; E69017; E69017.
KW Methanogenesis; Oxidoreductase; Multigene family.
FT INIT MET 0
FT NON_TER 0
SQ SEQUENCE 14 AA; 1557 MW; 97E9439C4223B871 CRC64;

Query Match 25.4%; Score 18; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPG 10
DB 6 YTPG 9

RESULT 35
ALL1_CYPDPO STANDARD; PRT; 8 AA.
ID ALL1_CYPDPO
AC P82152;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 1.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
CX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestri J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD_RES 8
FT MOD_RES 8
SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 23.9%; Score 17; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYPG 10
DB 3 HYNFG 7

RESULT 36
CCKN_MACEU STANDARD; PRT; 8 AA.
ID CCKN_MACEU
AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cholecystokinin (CCK).
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GN CCK.  
OS Macropus eugenii (Tamar wallaby), and  
OS Dasyurus viverrinus (Southeastern quoll).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.  
OX NCBI\_TaxID=9315, 9279;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=M.eugenii, and D.viverrinus;  
RC TISSUE=Brain;  
RX MEDLINE=88234141; PubMed=3375140;  
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;  
RT "Cholecystokinin octapeptide purified from brains of Australian  
marsupials."  
RL Peptides 9:429-431(1988).  
CC -!- FUNCTION: This peptide hormone induces gall bladder contraction  
and the release of pancreatic enzymes in the gut. Its function in  
the brain is not clear.  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR PIR; A43001; A43001.  
DR PIR; P00012; P00012.  
DR InterPro: IPR001651; Gastrin.  
DR PROSITE: PS00259; GASTRIN; 1.  
KW Amidation; Sulfation; Hormone.  
FT MOD\_RES 2 2 SULFATION.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 23.9%; Score 17; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 GW 11  
DB 4 GW 5

RESULT 37  
UP06\_MOUSE STANDARD; PRT; 8 AA.  
ID UP06\_MOUSE  
AC P38644;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Fibroblast;  
RX MEDLINE=95009907; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins  
using preparative two-dimensional gel electrophoresis."  
RL Electrophoresis 15:735-745(1994).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
protein is: 5.2, its MW is: 50 kDa.  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 817 MW; A35DD876676B05B1 CRC64;

Query Match 23.9%; Score 17; DB 1; Length 8;  
Best Local Similarity 60.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 HYPG 10  
DB 1 HSEPG 5

RESULT 38  
LMIP\_LOCMI

ID LMIP\_LOCMI STANDARD; PRT; 9 AA.  
AC P31799;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-OCT-1993 (Rel. 27, Last annotation update)  
DE Locustamyo-inhibiting peptide (LOM-MIP).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92179466; PubMed=1796179;  
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
RT "Isolation, identification and synthesis of locustamyo-inhibiting  
peptide (LOM-MIP), a novel biologically active neuropeptide from  
Locusta migratoria."  
RL Regul. Pept. 36:111-119(1991).  
CC -!- FUNCTION: Suppresses spontaneous contractions of the hindgut and  
oviduct.  
CC -!- TISSUE SPECIFICITY: Neurons located in two ventral cell clusters  
in the suboesophageal ganglion.  
DR PIR; A60065; AKIQIM.  
KW Amidation; Neuropeptide.  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1060 MW; 387D7DD4472AB6C3 CRC64;

Query Match 23.9%; Score 17; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 GW 11  
DB 8 GW 9

RESULT 39  
BPP\_VIPAS STANDARD; PRT; 10 AA.  
ID BPP\_VIPAS  
AC P31351;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide (Angiotensin-converting  
enzyme inhibitor).  
OS Vipera aspis (Aspic viper).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Viperinae; Vipera.  
OX NCBI\_TaxID=8706;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90382616; PubMed=2169439;  
RA Komori Y., Sugihara H.;  
RT "Characterization of a new inhibitor for angiotensin converting  
enzyme from the venom of Vipera aspis aspis."  
RL Int. J. Biochem. 22:767-771(1990).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
angiotensin-converting enzyme and enhances the action of  
bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; A60377; XASNPC.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match 23.9%; Score 17; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 GW 11



Db 2 GW 3

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RESULT 40
CA12_LITCI STANDARD; PRT; 10 AA.
ID CA12_LITCI
AC P82086;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 1.2/1.2Y4.
OS Litoria citropa (Australian blue mountains tree frog), and
OS Litoria splendida (Magnificent tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770, 30345;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEINS 1.2 AND 1.2Y4).
RC SPECIES=L.citropa; TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT mountains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry."
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
RN [2]
RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEIN 1.2).
RC SPECIES=L.splendida; TISSUE=Skin secretion;
RX MEDLINE=20069371; PubMed=10601876;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Smith B.P.;
RT "Differences in the skin peptides of the male and female Australian
RT tree frog Litoria splendida. The discovery of the aquatic male sex
RT pheromone splendipherin, together with Phe8 caerulein and the
RT antibiotic peptide caerin 1.10."
RL Eur. J. Biochem. 267:269-275(2000).
RN [1]
RP FUNCTION: Hypotensive neuropeptide (Probable).
RC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin dorsal glands.
CC -1- PTM: Isoform 1.2Y4 differs from isoform 1.2 in not being
CC sulfated.
CC -1- MASS SPECTROMETRY: MW=1366, METHOD=Electrospray.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1306 MW; 99DBFCD37861B5A CRC64;

Query Match 23.9%; Score 17; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GW 11
Db 6 GW 7
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OC Pelodyadinae; Litoria.
OX NCBI_TaxID=79697;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97374000; PubMed=9230483;
RA Steinboerner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
RA Ramsay S.L.;
RT "New caerin antibacterial peptides from the skin glands of the
RT Australian tree frog Litoria xanthomera."
RL J. Pept. Sci. 3:181-185(1997).
RN [1]
RP FUNCTION: Hypotensive neuropeptide.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=1354, METHOD=FAB.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1290 MW; 99DBF3837861B5A CRC64;

Query Match 23.9%; Score 17; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GW 11
Db 6 GW 7

RESULT 42
TKN1_SCYCA STANDARD; PRT; 10 AA.
ID TKN1_SCYCA
AC P08608;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Scyliorhinin I.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=86192829; PubMed=2422058;
RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.;
RT "Scyliorhinin I and II: two novel tachykinins from dogfish gut."
RL FEBS Lett. 200:111-116(1986).
RN [2]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazon N., Balmert R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
RT peptides from the brain of the dogfish, Scyliorhinus canicula."
RL Eur. J. Biochem. 214:469-474(1993).
RN [1]
RP FUNCTION: Tachykinins are active peptides which excite neurons,
RP evoke behavioral responses, are potent vasodilators and
RP secretagogues, and contract (directly or indirectly) many smooth
RP muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A24867; A24867.
DR InterPro; IPR002040; Tachy Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
```

SEQUENCE 10 AA; 1219 MW; D0602DB59C33AA9 CRC64;

Query Match 23.9%; Score 17; DB 1; Length 10;  
Best Local Similarity 75.0%; Pred. No. 3.8e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYG 8  
DB 5 KFYG 8

## RESULT 43

TKS1\_AEDAE

ID TKS1\_AEDAE STANDARD; PRT; 10 AA.

AC P42634;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Sialokinin I.

OS Aedes aegypti (Yellowfever mosquito).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.

OX NCBI\_TaxID=7159;

RN [1]

RP SEQUENCE.

RC STRAIN=Rockefeller; TISSUE=Salivary gland;

RX MEDLINE=94105119; PubMed=8278354;

RA Champagne D.E., Ribeiro J.M.C.;

RT "Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito Aedes aegypti.";

RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).

CC -!- FUNCTION: Vasodilatory peptide. May activate macrophages at the site of feeding.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PIR; A49581; A49581.

DR InterPro; IPR002040; Tachy Neurokinin.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation.

FT MOD RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1145 MW; 3DCFD6B59C33AA8 CRC64;

Query Match 23.9%; Score 17; DB 1; Length 10;  
Best Local Similarity 75.0%; Pred. No. 3.8e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYG 8  
DB 5 KFYG 8

## RESULT 44

TKS2\_AEDAE

ID TKS2\_AEDAE STANDARD; PRT; 10 AA.

AC P42635;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Sialokinin II.

OS Aedes aegypti (Yellowfever mosquito).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.

OX NCBI\_TaxID=7159;

RN [1]

RP SEQUENCE.

RC STRAIN=Rockefeller; TISSUE=Salivary gland;

RX MEDLINE=94105119; PubMed=8278354;

RA Champagne D.E., Ribeiro J.M.C.;

RT "Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito Aedes aegypti.";

RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).

CC -!- FUNCTION: Vasodilatory peptide. May activate macrophages at the site of feeding.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PIR; B49581; B49581.

DR InterPro; IPR002040; Tachy Neurokinin.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation.

FT MOD RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1146 MW; 3DC77C6B59C33AA8 CRC64;

Query Match 23.9%; Score 17; DB 1; Length 10;  
Best Local Similarity 75.0%; Pred. No. 3.8e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KHYG 8  
DB 5 KFYG 8

## RESULT 45

UXA6\_CHLTR

ID UXA6\_CHLTR STANDARD; PRT; 10 AA.

AC P38007;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Unknown protein from 2D-page from elementary body (Fragment).

OS Chlamydia trachomatis.

OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI\_TaxID=813;

RN [1]

RP SEQUENCE.

RC STRAIN=12/434/Bu;

RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,

RA Comanducci M., Christianen G., Birkelund S., Viretton E., Ratti G.,

RA Pallini V.;

RL Submitted (SEP-1994) to Swiss-Prot.

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 6.44, ITS MW IS: 38.6 kDa.

DR SIENA-2DPAGE; P38007; -.

FT NON TER 10 10

Query Match 23.9%; Score 17; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFK 3  
DB 2 NFK 4

Search completed: August 30, 2004, 10:50:21  
Job time : 2.89527 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 3.30743 Seconds  
(without alignments)  
319.918 Million cell updates/sec

Title: US-09-720-469A-5  
Perfect score: 71  
Sequence: 1 NFKLKHVPGW 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID     | Description        |
|------------|-------|-------------|--------|----|--------|--------------------|
| 1          | 28    | 39.4        | 8      | 2  | A61348 | red pigment-concen |
| 2          | 28    | 39.4        | 10     | 2  | A60421 | hypertrehalosemic  |
| 3          | 28    | 39.4        | 10     | 2  | S08997 | hypertrehalosemic  |
| 4          | 28    | 39.4        | 10     | 2  | S08998 | hypertrehalosemic  |
| 5          | 28    | 39.4        | 10     | 2  | A26381 | hypertrehalosemic  |
| 6          | 26    | 36.6        | 8      | 2  | S55310 | adipokinetic hormo |
| 7          | 26    | 36.6        | 8      | 2  | A58620 | adipokinetic hormo |
| 8          | 26    | 36.6        | 10     | 1  | RHAQ2  | gonadoliberin II - |
| 9          | 26    | 36.6        | 10     | 1  | A61126 | gonadoliberin II - |
| 10         | 26    | 36.6        | 10     | 2  | B46030 | gonadoliberin I -  |
| 11         | 26    | 36.6        | 10     | 2  | S15422 | adipokinetic hormo |
| 12         | 25    | 35.2        | 8      | 2  | A33995 | adipokinetic hormo |
| 13         | 25    | 35.2        | 8      | 2  | A58641 | adipokinetic hormo |
| 14         | 25    | 35.2        | 8      | 2  | S21653 | neuropeptide - flo |
| 15         | 25    | 35.2        | 10     | 2  | B33995 | hypotrehalosemic h |
| 16         | 25    | 35.2        | 10     | 2  | A21114 | gonadoliberin - ch |
| 17         | 25    | 35.2        | 10     | 2  | S39030 | lysyl-bradykinin - |
| 18         | 24    | 33.8        | 10     | 2  | S70338 | napin small chain  |
| 19         | 24    | 33.8        | 11     | 2  | PH1322 | Ig heavy chain DJ  |
| 20         | 24    | 33.8        | 14     | 2  | PT0288 | Ig heavy chain CRD |
| 21         | 23    | 32.4        | 9      | 2  | S65388 | cytochrome-c oxida |
| 22         | 23    | 32.4        | 10     | 2  | PT0302 | Ig heavy chain CRD |
| 23         | 23    | 32.4        | 11     | 2  | S08995 | hypertrehalosemic  |
| 24         | 23    | 32.4        | 8      | 2  | A49823 | adipokinetic hormo |
| 25         | 22    | 31.0        | 8      | 2  | A44960 | neuropeptide led-C |
| 26         | 22    | 31.0        | 8      | 2  | A43976 | hypertrehalosemic  |
| 27         | 22    | 31.0        | 8      | 2  | B43976 | hypertrehalosemic  |
| 28         | 22    | 31.0        | 8      | 2  |        |                    |
| 29         | 22    | 31.0        | 8      | 2  |        |                    |

|    |    |      |    |   |        |                    |
|----|----|------|----|---|--------|--------------------|
| 30 | 22 | 31.0 | 8  | 2 | A05169 | neuropeptide M-I - |
| 31 | 22 | 31.0 | 10 | 1 | RHMG3  | gonadoliberin - se |
| 32 | 22 | 31.0 | 10 | 2 | S53789 | neuropeptide Pec-H |
| 33 | 22 | 31.0 | 11 | 2 | S05002 | corazonin - Americ |
| 34 | 22 | 31.0 | 13 | 2 | A60409 | bombesin-like pept |
| 35 | 22 | 31.0 | 13 | 2 | S23640 | Ig kappa chain J s |
| 36 | 22 | 31.0 | 14 | 2 | S33802 | chaperone, TCP1-re |
| 37 | 21 | 29.6 | 11 | 2 | PT0209 | T-cell receptor al |
| 38 | 21 | 29.6 | 13 | 2 | PH1593 | Ig H chain V-D-J r |
| 39 | 21 | 29.6 | 14 | 2 | S03530 | Ig heavy chain J r |
| 40 | 20 | 28.2 | 8  | 2 | A28004 | adipokinetic hormo |
| 41 | 20 | 28.2 | 8  | 2 | S10596 | adipokinetic hormo |
| 42 | 20 | 28.2 | 8  | 2 | S11545 | adipokinetic hormo |
| 43 | 20 | 28.2 | 8  | 2 | PT0368 | Ig gamma chain C r |
| 44 | 20 | 28.2 | 12 | 2 | PQ0786 | NADH2 dehydrogenas |
| 45 | 20 | 28.2 | 14 | 2 | PQ0152 | 18k iron-sulfur pr |

## ALIGNMENTS

RESULT 1  
A61348  
red pigment-concentrating hormone - northern shrimp  
N/Alternate names: blanching hormone  
C/Species: Pandalus borealis (northern shrimp)  
C/Date: 02-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C/Accession: A61348; S07139  
R/Fernlund, P.; Josefsson, L.  
Science 177, 173-175, 1972  
A/Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.  
A/Reference number: A61348; MUID:72228738; PMID:5041363  
A/Accession: A61348  
A/Molecule type: protein  
A/Residues: 1-8 <FER1>  
R/Fernlund, P.  
Biochim. Biophys. Acta 371, 304-311, 1974  
A/Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus bore  
A/Reference number: S07139; MUID:75054965; PMID:4433569  
A/Accession: S07139  
A/Molecule type: protein  
A/Residues: 'E', 2-8 <FER2>  
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C/Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pi  
zed pigment-containing cells.  
C/Superfamily: adipokinetic hormone  
C/Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutami  
F,I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F,I/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 39.4%; Score 28; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYGPGW 11  
DB 3 NFSPGW 8

RESULT 2  
A60421  
hypertrehalosemic hormone - German cockroach  
N/Alternate names: Bld-BrTH  
C/Species: Blattella germanica (German cockroach)  
C/Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 31-Oct-1997  
C/Accession: A60421; S09137  
R/Veenstra, J.A.; Camps, F.  
Neuropeptides 15, 107-109, 1990  
A/Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, Blatte  
A/Reference number: A60421; MUID:91179584; PMID:2080017  
A/Accession: A60421  
A/Molecule type: protein  
A/Residues: 1-10 <VEB>

R;Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment  
A;Reference number: S08995; MUID:90253659; PMID:2340112  
A;Accession: S09137  
A;Molecule type: protein  
A;Residues: 1-10 <GAE>  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 39.4%; Score 28; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 HYPGW 11  
:: |||  
Db 3 NFSPGW 8

RESULT 3  
S08997  
hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)  
C;Species: Gromphadorina portentosa  
C;Date: 30-Jun-1992 #sequence\_revision 14-Sep-1994 #text\_change 24-Oct-1997  
C;Accession: S08997  
R;Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment  
A;Reference number: S08995; MUID:90253659; PMID:2340112  
A;Accession: S08997  
A;Molecule type: protein  
A;Residues: 1-10 <GAE>  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 39.4%; Score 28; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 HYPGW 11  
:: |||  
Db 3 NFSPGW 8

RESULT 4  
S08998  
hypertrehalosemic neuropeptide Bld-HrTH - Madeira cockroach  
C;Species: Leucophaea maderae (Madeira cockroach)  
C;Date: 30-Jun-1992 #sequence\_revision 14-Sep-1994 #text\_change 24-Oct-1997  
C;Accession: S08998  
R;Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment  
A;Reference number: S08995; MUID:90253659; PMID:2340112  
A;Accession: S08998  
A;Molecule type: protein  
A;Residues: 1-10 <GAE>  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 39.4%; Score 28; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 HYPGW 11  
:: |||  
Db 3 NFSPGW 8

RESULT 5  
A26381  
hypertrehalosemic hormone - gray cockroach  
C;Species: Nauphoeta cinerea (gray cockroach)  
C;Date: 31-Mar-1988 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997  
C;Accession: A26381  
R;Gaede, G.; Rinehart Jr., K.L.  
Biochem. Biophys. Res. Commun. 141, 774-781, 1986  
A;Title: Amino acid sequence of a hypertrehalosaemic neuropeptide from the corpus cardia  
A;Reference number: A26381; MUID:87100208; PMID:3801028  
A;Accession: A26381  
A;Molecule type: protein  
A;Residues: 1-10 <GAD>  
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 39.4%; Score 28; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 HYPGW 11  
:: |||  
Db 3 NFSPGW 8

RESULT 6  
S55310  
adipokinetic hormone - damselfly (Pseudagrion inconspicuum)  
N;Alternate names: Psi-AKH  
C;Species: Pseudagrion inconspicuum  
C;Date: 19-Mar-1997 #sequence\_revision 31-Oct-1997 #text\_change 07-May-1999  
C;Accession: S55310  
R;Janssens, M.P.E.; Kellner, R.; Gaede, G.  
Biochem. J. 302, 539-543, 1994  
A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicuum  
A;Reference number: S55310; MUID:94379987; PMID:8093008  
A;Accession: S55310  
A;Molecule type: protein  
A;Residues: 1-8 <JAN>  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.6%; Score 26; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 HYPGW 11  
:: |||  
Db 3 NFSPGW 8

RESULT 7  
A58620  
adipokinetic hormone - damselfly (Ischnura senegalensis)  
C;Species: Ischnura senegalensis  
C;Date: 28-Oct-1997 #sequence\_revision 31-Oct-1997 #text\_change 07-May-1999  
C;Accession: A58620  
R;Janssens, M.P.E.; Kellner, R.; Gaede, G.  
Biochem. J. 302, 539-543, 1994  
A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicuum  
A;Reference number: S55310; MUID:94379987; PMID:8093008  
A;Accession: A58620  
A;Molecule type: protein

A/Residues: 1-8 <JAN>  
 C/Superfamily: adipokinetic hormone  
 C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 36.6%; Score 26; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 HXPGW 11  
 : : : :  
 Db 3 NFTPWG 8

## RESULT 8

RHAQ2  
 gonadoliberin II - American alligator  
 N/Alternate names: gonadotropin-releasing hormone II  
 C/Species: Alligator mississippiensis (American alligator)  
 C/Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 18-Mar-1997  
 C/Accession: B60066  
 R/Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson  
 Regul. Pept. 33, 105-116, 1991  
 A/Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of  
 A/Reference number: A60066; MUID:91352338; PMID:1882082  
 A/Accession: B60066  
 A/Molecule type: protein  
 A/Residues: 1-10 <LOV>  
 C/Superfamily: gonadoliberin  
 C/Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F/10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 36.6%; Score 26; DB 1; Length 10;  
 Best Local Similarity 42.9%; Pred. No. 2.9e+02;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 KHYPGW 11  
 : : : :  
 Db 1 QHWSHG 7

## RESULT 9

A61126  
 gonadoliberin - spotted ratfish  
 N/Alternate names: gonadotropin-releasing hormone  
 C/Species: Hydrolagus collieri (spotted ratfish)  
 C/Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 18-Mar-1997  
 C/Accession: A61126  
 R/Lovejoy, D.A.; Sherwood, N.M.; Fischer, W.H.; Jackson, B.C.; Rivier, J.E.; Lee, T.  
 Gen. Comp. Endocrinol. 82, 152-161, 1991  
 A/Title: Primary structure of gonadotropin-releasing hormone from the brain of a holocope  
 A/Reference number: A61126; MUID:91340067; PMID:1678723  
 A/Accession: A61126  
 A/Molecule type: protein  
 A/Residues: 1-10 <LOV>  
 A/Experimental source: brain  
 C/Superfamily: gonadoliberin  
 C/Keywords: amidated carboxyl end; brain; hormone; pyroglutamic acid  
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F/10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 36.6%; Score 26; DB 1; Length 10;  
 Best Local Similarity 42.9%; Pred. No. 2.9e+02;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 KHYPGW 11  
 : : : :  
 Db 1 QHWSHG 7

## RESULT 10

B46030  
 gonadoliberin II - spiny dogfish  
 N/Alternate names: gonadotropin-releasing hormone  
 C/Species: Squalus acanthias (spiny dogfish)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Jan-2003  
 C/Accession: B46030  
 R/Lovejoy, D.A.; Fischer, W.H.; Ngamvongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter, R.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992  
 A/Title: Distinct sequence of gonadotropin-releasing hormone (GnRH) in dogfish brain pro  
 A/Reference number: A46030; MUID:92335300; PMID:1631133  
 A/Accession: B46030  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-10 <LOV>  
 C/Superfamily: gonadoliberin  
 C/Keywords: hormone; pyroglutamic acid  
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 36.6%; Score 26; DB 2; Length 10;  
 Best Local Similarity 42.9%; Pred. No. 2.9e+02;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 KHYPGW 11  
 : : : :  
 Db 1 QHWSHG 7

## RESULT 11

A46030  
 gonadoliberin I - spiny dogfish  
 N/Alternate names: gonadotropin-releasing hormone  
 C/Species: Squalus acanthias (spiny dogfish)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Dec-1998  
 C/Accession: A46030  
 R/Lovejoy, D.A.; Fischer, W.H.; Ngamvongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter, R.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992  
 A/Title: Distinct sequence of gonadotropin-releasing hormone (GnRH) in dogfish brain pro  
 A/Reference number: A46030; MUID:92335300; PMID:1631133  
 A/Accession: A46030  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-10 <LOV>  
 C/Keywords: hormone; pyroglutamic acid  
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 36.6%; Score 26; DB 2; Length 10;  
 Best Local Similarity 42.9%; Pred. No. 2.9e+02;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 KHYPGW 11  
 : : : :  
 Db 1 QHWSHG 7

## RESULT 12

S15422  
 adipokinetic hormone - cockchafer  
 C/Species: Melolontha melolontha (cockchafer)  
 C/Date: 19-Mar-1997 #sequence\_revision 31-Oct-1997 #text\_change 31-Oct-1997  
 C/Accession: S15422  
 R/Gaede, G.  
 Biochem. J. 275, 671-677, 1991  
 A/Title: A unique charged tyrosine-containing member of the adipokinetic hormone/red-p  
 A/Reference number: S15422; MUID:91248100; PMID:2039445  
 A/Accession: S15422  
 A/Molecule type: protein  
 A/Residues: 1-8 <BIO>  
 C/Superfamily: adipokinetic hormone  
 C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 35.2%; Score 25; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPGW 11  
: |||  
Db 3 NYSPDW 8

## RESULT 13

A33995

adipokinetic hormone - black horse fly

C/Species: Tabanus atratus (black horse fly)

C/Date: 23-Mar-1990 #sequence\_revision 23-Mar-1990 #text\_change 31-Oct-1997

C/Accession: A33995

R/Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989

A/Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehal

A/Reference number: A33995; PMID:90046758; PMID:2813385

A/Accession: A33995

A/Molecule type: protein

A/Residues: 1-8 &lt;JAF&gt;

C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

F/8/Modified site: amidated carboxyl end (Trp) #status predicted

## Query Match

Best Local Similarity 35.2%; Score 25; DB 2; Length 8;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGW 11  
: |||  
Db 4 FTPGW 8

## RESULT 14

A58641

adipokinetic hormone - dor beetle

C/Species: Geotrupes stercorosus (dor beetle)

C/Date: 28-Oct-1997 #sequence\_revision 31-Oct-1997 #text\_change 31-Oct-1997

C/Accession: A58641

R/Gaede, G. Biochem. J. 275, 671-677, 1991

A/Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red-pi

A/Reference number: S15422; PMID:91248100; PMID:2039445

A/Accession: A58641

A/Molecule type: protein

A/Residues: 1-8 &lt;BIO&gt;

C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8/Modified site: amidated carboxyl end (Trp) #status experimental

## Query Match

Best Local Similarity 35.2%; Score 25; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPGW 11  
: |||  
Db 3 NYSPDW 8

## RESULT 15

S21663

neuropeptide - flower beetle (Pachnoda marginata)

C/Species: Pachnoda marginata

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997

C/Accession: S21663

R/Gaede, G.; Lopata, A.; Kellner, R.; Rinehart, K.L. Biol. Chem. Hoppe-Seyler 373, 133-142, 1992

A/Title: Chem. Hoppe-Seyler 373, 133-142, 1992

A/Title: Primary structures of neuropeptides isolated from the corpora cardiaca of vari

ectrometry. A/Reference number: S21663; PMID:92265187; PMID:1586453

A/Accession: S21663  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-8 <GAE>

Query Match 35.2%; Score 25; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPGW 11  
: |||  
Db 3 NYSPDW 8

## RESULT 16

B33995

hypotrehalosemic hormone - black horse fly

C/Species: Tabanus atratus (black horse fly)

C/Date: 23-Mar-1990 #sequence\_revision 23-Mar-1990 #text\_change 31-Oct-1997

C/Accession: B33995

R/Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989

A/Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehal

A/Reference number: A33995; PMID:90046758; PMID:2813385

A/Accession: B33995

A/Molecule type: protein

A/Residues: 1-10 &lt;JAF&gt;

C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

F/10/Modified site: amidated carboxyl end (Tyr) #status predicted

Query Match 35.2%; Score 25; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 4.3e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGW 11  
: |||  
Db 4 FTPGW 8

## RESULT 17

A21114

gonadoliberin - chum salmon

C/Species: Oncorhynchus keta (chum salmon)

C/Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 18-Jun-1993

C/Accession: A21114

R/Sherwood, N.; Elden, L.; Brownstein, M.; Spiess, J.; Rivier, J.; Vale, W. Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983

A/Title: Characterization of a teleost gonadotropin-releasing hormone.

A/Reference number: A21114; PMID:83195140; PMID:6341999

A/Accession: A21114

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 &lt;SHE&gt;

Query Match 35.2%; Score 25; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 4.3e+02;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYPGW 11  
: |||  
Db 1 QHWSYGM 7

## RESULT 18

S39030

lysyl-bradykinin - rainbow trout

C/Species: Oncorhynchus mykiss (rainbow trout)

C/Date: 19-May-1994 #sequence\_revision 19-Apr-1996 #text\_change 18-Aug-2000

C/Accession: S39030

R/Conlon, J.M.; Olson, K.R. FEBS Lett. 334, 75-78, 1993

A/Title: Purification of a vasoactive peptide related to lysyl-bradykinin from trout pla  
A/Reference number: S39030; MUID:94039817; PMID:8224232  
A/Accession: S39030  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <CON>  
C/Superfamily: unassigned animal peptides

Query Match 33.8%; Score 24; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YGPGW 11  
|||  
Db 4 PGW 6

## RESULT 19

S70338  
napin small chain S3A - Swedish turnip (fragment)  
C/Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)  
C/Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-May-1999  
C/Accession: S70338  
R/Neumann, G.M.; Condron, R.; Thomas, I.; Polya, G.M.  
Biochim. Biophys. Acta 1295, 23-33, 1996  
A/Title: Purification and sequencing of multiple forms of Brassica napus seed napin small  
A/Reference number: S70336; MUID:96283790; PMID:8679670  
A/Accession: S70338  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-11 <NEU>

Query Match 33.8%; Score 24; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 6.9e+02;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 GPGW 11  
|||  
Db 8 GPSW 11

## RESULT 20

PH1322  
Ig heavy chain DJ region (clone C344-99) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1322  
R/Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH1322  
A/Molecule type: DNA  
A/Residues: 1-14 <WAS>  
C/Keywords: heterotetramer; immunoglobulin

Query Match 33.8%; Score 24; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 8.8e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGW 11  
: |||  
Db 2 WGS GW 6

## RESULT 21

PT0288  
Ig heavy chain CRD3 region (clone 4-106) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0288  
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jo  
A/Reference number: PT0222; MUID:91108337; PMID:1899102  
A/Accession: PT0288  
A/Molecule type: DNA  
A/Residues: 1-9 <YAM>  
A/Experimental source: B lymphocyte  
C/Keywords: heterotetramer; immunoglobulin

Query Match 32.4%; Score 23; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 YGPGW 11  
|||  
Db 5 YSSGW 9

## RESULT 22

S65388  
cytochrome-c oxidase (EC 1.9.3.1) chain VII c, hepatic - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
C/Accession: S65388; S65389  
R/Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.  
Eur. J. Biochem. 230, 235-241, 1995  
A/Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term  
A/Reference number: S65372; MUID:95324529; PMID:7601105  
A/Accession: S65388  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <SCH>  
A/Accession: S65389  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <SC2>  
C/Superfamily: cytochrome-c oxidase chain VIIC  
C/Keywords: oxidoreductase

Query Match 32.4%; Score 23; DB 2; Length 10;  
Best Local Similarity 71.4%; Pred. No. 9.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 6 HY--GPG 10  
|||  
Db 2 HYE GPG 8

## RESULT 23

S77990  
cytochrome-c oxidase (EC 1.9.3.1) chain VIIC - bigeye tuna (fragment)  
C/Species: Thunnus obesus (bigeye tuna)  
C/Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 30-Jan-1998  
C/Accession: S77990  
R/Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.  
submitted to the Protein Sequence Database, June 1997  
A/Reference number: S77980  
A/Accession: S77990  
A/Molecule type: protein  
A/Residues: 1-10 <ARN>  
A/Experimental source: heart; liver  
C/Genetics:  
A/Genome: nuclear  
C/Function:  
A/Pathway: oxidative phosphorylation; respiratory chain  
C/Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 32.4%; Score 23; DB 2; Length 10;  
Best Local Similarity 71.4%; Pred. No. 9.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 6 HY--GPG 10  
|||  
Db 2 HYAEGPG 8

RESULT 24

PT0302  
 1g heavy chain CRD3 region (clone 5-112) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C/Accession: PT0302  
 R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
 A/Reference number: PT0222; MUID:91108337; PMID:1899102  
 A/Accession: PT0302  
 A/Molecule type: DNA  
 A/Residues: 1-11 <YAM>  
 A/Experimental source: B lymphocyte  
 C/Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 32.4%; Score 23; DB 2; Length 11;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 YGPGW 11  
 DB 6 YSSGW 10

RESULT 25

S08995  
 hypertrehalosemic hormone I - oriental cockroach  
 N/Alternate names: Pea-CAH-I  
 C/Species: Blatta orientalis (oriental cockroach)  
 C/Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997  
 C/Accession: S08995  
 R/Gaede, G.; Rinehart, K.L.  
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
 A/Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora  
 entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard  
 A/Reference number: S08995; MUID:90253659; PMID:2340112  
 A/Accession: S08995  
 A/Molecule type: protein  
 A/Residues: 1-8 <GAE>  
 A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
 C/Superfamily: adipokinetic hormone  
 C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
 F,1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F,8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 31.0%; Score 22; DB 2; Length 8;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYPGW 11  
 DB 3 NFSPNW 8

RESULT 26

A49823  
 adipokinetic hormone I - American cockroach  
 N/Alternate names: periplanetin CC-1  
 C/Species: Periplaneta americana (American cockroach)  
 C/Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
 C/Accession: A49823  
 R/Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984  
 A/Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp  
 A/Reference number: A49823; MUID:84298179; PMID:6591205  
 A/Accession: A49823  
 A/Molecule type: protein  
 A/Residues: 1-8 <SCA>  
 C/Superfamily: adipokinetic hormone  
 C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F,1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F,8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 31.0%; Score 22; DB 2; Length 8;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYPGW 11  
 DB 3 NFSPNW 8

RESULT 27

A44960  
 neuropeptide led-CC-1 - Colorado potato beetle  
 C/Species: Leptinotarsa decemlineata (Colorado potato beetle)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C/Accession: A44960  
 R/Gaede, G.; Kellner, R.  
 Peptides 10, 1287-1289, 1989  
 A/Title: The metabolic neuropeptides of the corpus cardiaca from the potato beetle and t  
 A/Reference number: A44960; MUID:90160053; PMID:2576128  
 A/Accession: A44960  
 A/Molecule type: protein  
 A/Residues: 1-8 <GAE>  
 C/Superfamily: adipokinetic hormone  
 C/Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
 F,1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F,8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match

Best Local Similarity 31.0%; Score 22; DB 2; Length 8;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYPGW 11  
 DB 3 NFSPNW 8

RESULT 28

A43976  
 hypertrehalosemic hormone - yellow mealworm  
 C/Species: Tenebrio molitor (yellow mealworm)  
 C/Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 07-May-1999  
 C/Accession: A43976  
 R/Gaede, G.; Rosinski, G.  
 Peptides 11, 455-459, 1990  
 A/Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid bee  
 A/Reference number: A43976; MUID:90341081; PMID:2381871  
 A/Accession: A43976  
 A/Molecule type: protein  
 A/Residues: 1-8 <GAE>  
 C/Superfamily: adipokinetic hormone  
 C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
 F,1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F,8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 31.0%; Score 22; DB 2; Length 8;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYPGW 11  
 DB 3 NFSPNW 8

RESULT 29

B43976  
 hypertrehalosemic hormone - beetle (Zophobas rugipes)  
 C/Species: Zophobas rugipes  
 C/Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 07-May-1999  
 C/Accession: B43976  
 R/Gaede, G.; Rosinski, G.



Peptides 11, 455-459, 1990

A/Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetles  
A/Reference number: A43976; MUID:90341061; PMID:2381871  
A/Accession: B43976  
A/Molecule type: protein  
A/Residues: 1-8 <GAE>  
C/Superfamily: adipokinetic hormone  
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 31.0%; Score 22; DB 2; Length 8;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 HYPGW 11  
: : :  
Db 3 NFSPW 8

RESULT 30

A05169

neuropeptide M-1 - American cockroach  
C/Species: Periplaneta americana (American cockroach)  
C/Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Dec-1993  
C/Accession: A05169  
R/Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.  
Biochem. Biophys. Res. Commun. 124, 350-358, 1984  
A/Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry  
A/Reference number: A90118; MUID:85046530; PMID:6548628  
A/Accession: A05169  
A/Molecule type: protein  
A/Residues: 1-8 <MT>  
C/Keywords: neuropeptide

Query Match 31.0%; Score 22; DB 2; Length 8;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 HYPGW 11  
: : :  
Db 3 NFSPW 8

RESULT 31

RHMGs

gonadoliberin - sea lamprey  
N/Alternate names: gonadotropin releasing hormone (GNRH)  
C/Species: Petromyzon marinus (sea lamprey)  
C/Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 18-Mar-1997  
C/Accession: A01412  
R/Sherwood, N.M.; Sower, S.A.; Marshak, D.R.; Fraser, B.A.; Brownstein, M.J.  
J. Biol. Chem. 261, 4812-4819, 1986  
A/Title: Primary structure of gonadotropin-releasing hormone from lamprey brain.  
A/Reference number: A01412; MUID:86168192; PMID:3514603  
A/Accession: A01412  
A/Molecule type: protein  
A/Residues: 1-10 <SHE>  
C/Comment: This hormone was isolated from the brain.  
C/Superfamily: gonadoliberin  
C/Keywords: amidated carboxyl end; hormone; pyroglutamic acid  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F/10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 31.0%; Score 22; DB 1; Length 10;  
Best Local Similarity 42.9%; Pred. No. 1.4e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 KHYPGW 11  
: : :  
Db 1 QHYSLEW 7

RESULT 32

S53789

neuropeptide Pec-HrTH - Platyleura capensis  
C/Species: Platyleura capensis  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 07-May-1999  
C/Accession: S53789  
R/Gaede, G.; Janssens, M.P.E.  
Biol. Chem. Hoppe-Seyler 375, 803-809, 1994  
A/Title: Cicadas contain novel members of the AXH/RPCH family peptides with hypertrehalosemic activity  
A/Reference number: S53789; MUID:95225985; PMID:7710694  
A/Accession: S53789  
A/Molecule type: protein  
A/Residues: 1-10 <GAE>  
C/Keywords: blocked amino end; blocked carboxyl end

Query Match 31.0%; Score 22; DB 2; Length 10;  
Best Local Similarity 33.3%; Pred. No. 1.4e+03;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 HYPGW 11  
: : :  
Db 3 NFSPW 8

RESULT 33

S05002

corazonin - American cockroach  
C/Species: Periplaneta americana (American cockroach)  
C/Date: 07-Sep-1990 #sequence\_revision 09-Apr-1998 #text\_change 09-Apr-1998  
C/Accession: S05002  
R/Veenstra, J.A.  
FEBS Lett. 250, 231-234, 1989  
A/Title: Isolation and structure of corazonin, a cardioactive peptide from the american cockroach  
A/Reference number: S05002; MUID:89325572; PMID:2753132  
A/Accession: S05002  
A/Molecule type: protein  
A/Residues: 1-11 <VEE>  
C/Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F/11/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 31.0%; Score 22; DB 2; Length 11;  
Best Local Similarity 60.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 YGPGW 11  
: : :  
Db 5 YSRGW 9

RESULT 34

A60409

bombesin-like peptide L - frog (Pseudophryne guentheri)  
C/Species: Pseudophryne guentheri  
C/Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2000  
C/Accession: A60409  
R/Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior  
Peptides 11, 299-304, 1990  
A/Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australia  
A/Reference number: A60409; MUID:90287814; PMID:2356157  
A/Accession: A60409  
A/Molecule type: protein  
A/Residues: 1-13 <SIM>  
C/Superfamily: unassigned animal peptides  
C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F/13/Modified site: pyrrolidone carboxylic acid (Met) #status experimental

Query Match 31.0%; Score 22; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 GPGW 11

Db 4 GPQW 7

## RESULT 35

S23640

Ig kappa chain J segment (J-kappa-3) - human

C:Species: Homo sapiens (man)

C&gt;Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996

C:Accession: S23640

R:Huber, C.; Klobbeck, H.G.; Zachau, H.G.

Eur. J. Immunol. 22, 1561-1565, 1992

A&gt;Title: Ongoing V(kappa)-J(kappa) recombination after formation of a productive V(kappa)

A:Reference number: S23637; MUID:92289816; PMID:1601042

A:Accession: S23640

A&gt;Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-13 &lt;HUB&gt;

A:Cross-references: EMBL:X63370

A&gt;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991

C:Keywords: heterotetramer; immunoglobulin

## Query Match

Best Local Similarity 31.0%; Score 22; DB 2; Length 13;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 YGPG 10

Db 3 FGPG 6

## RESULT 36

S33802

chaperone, TCPI-related - oat

C:Species: Avena sativa (oat)

C&gt;Date: 02-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 17-Mar-1999

C:Accession: S33802

R:Mumert, E.; Grimm, R.; Specht, V.; Eckerskorn, C.; Schiltz, E.; Gatenby, A.A.; Schaefer

Nature 363, 644-648, 1993

A&gt;Title: A TCPI-related molecular chaperone from plants refolds phytochrome to its photo

A:Reference number: S33800; MUID:93288140; PMID:8099715

A:Accession: S33802

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 &lt;MUM&gt;

## Query Match

Best Local Similarity 31.0%; Score 22; DB 2; Length 14;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 GPGW 11

Db 8 GPWW 11

## RESULT 37

PT0209

T-cell receptor alpha chain V-J region (4-1-L.6) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997

C:Accession: PT0209

R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A&gt;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted

A:Reference number: PT0209; MUID:91217621; PMID:1902501

A:Accession: PT0209

A:Molecule type: mRNA

A:Residues: 1-11 &lt;NAK&gt;

C:Keywords: T-cell receptor

## Query Match

Best Local Similarity 29.6%; Score 21; DB 2; Length 11;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HYG 8  
Db 6 HYG 8

## RESULT 38

PH1593

Ig H chain V-D-J region (wild-type clone 144) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C&gt;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C:Accession: PH1593

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A&gt;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A:Reference number: PH1580; MUID:93301609; PMID:8315387

A:Accession: PH1593

A:Molecule type: DNA

A:Residues: 1-13 &lt;LEV&gt;

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

## Query Match

Best Local Similarity 29.6%; Score 21; DB 2; Length 13;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LKHY 7

Db 5 LRHY 8

## RESULT 39

S03530

Ig heavy chain J region (JH-4) - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C&gt;Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 21-Jul-2000

C:Accession: S03530

R:Schwager, J.; Grosberger, D.; du Pasquier, L.

EMBO J. 7, 2409-2415, 1988

A&gt;Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus

A:Reference number: S01158; MUID:89052653; PMID:2903824

A:Accession: S03530

A:Molecule type: DNA

A:Residues: 1-14 &lt;SCH&gt;

A:Cross-references: EMBL:X14918; NID:964805; PIDD:CAA33043.1; PID:gl334657

## Query Match

Best Local Similarity 29.6%; Score 21; DB 2; Length 14;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYPG 10

Db 3 HMGQG 7

## RESULT 40

A28004

adipokinetin hormone G - two-spotted cricket

N:Alternate names: AKH-G

C:Species: Gryllus bimaculatus (two-spotted cricket)

C&gt;Date: 30-Jun-1989 #sequence\_revision 24-Oct-1997 #text\_change 24-Oct-1997

C:Accession: A28004

R:Gaede, G.; Rinehart, K.L.

Biochem. Biophys. Res. Commun. 149, 908-914, 1987

A&gt;Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptidic

A:Reference number: A28004; MUID:88106553; PMID:3426616

A:Accession: A28004

A:Molecule type: protein

A:Residues: 1-8 &lt;GAE&gt;

A&gt;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C:Superfamily: adipokinetin hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental





Db 7 EFKNYG 12

Search completed: August 30, 2004, 10:58:50  
Job time : 4.30743 secs

---

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 13.4527 Seconds  
(without alignments)  
257.253 Million cell updates/sec

Title: US-09-720-469A-5  
Perfect score: 71  
Sequence: 1 NFKLKHYPGW 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 149443

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                 | Description        |
|------------|-------|-------------|--------|--------------------|--------------------|
| 1          | 45    | 63.4        | 14     | US-10-394-980-52   | Sequence 52, Appl  |
| 2          | 36    | 50.7        | 13     | US-10-038-612-168  | Sequence 168, App  |
| 3          | 31    | 43.7        | 8      | US-09-849-092-2    | Sequence 2, Appl   |
| 4          | 31    | 43.7        | 11     | US-09-791-551-99   | Sequence 99, Appl  |
| 5          | 30    | 42.3        | 8      | US-09-880-748-2870 | Sequence 2870, Ap  |
| 6          | 30    | 42.3        | 8      | US-10-293-418-2870 | Sequence 2870, Ap  |
| 7          | 30    | 42.3        | 11     | US-10-169-710-23   | Sequence 23, Appl  |
| 8          | 30    | 42.3        | 13     | US-10-038-612-169  | Sequence 169, Appl |
| 9          | 30    | 42.3        | 13     | US-10-239-321A-52  | Sequence 52, Appl  |
| 10         | 29    | 40.8        | 10     | US-10-450-036A-95  | Sequence 95, Appl  |
| 11         | 28    | 39.4        | 8      | US-09-910-552-37   | Sequence 37, Appl  |
| 12         | 28    | 39.4        | 8      | US-10-643-465-37   | Sequence 37, Appl  |
| 13         | 28    | 39.4        | 10     | US-10-072-419-2    | Sequence 2, Appl   |
| 14         | 27    | 38.0        | 9      | US-10-013-312-41   | Sequence 41, Appl  |
| 15         | 27    | 38.0        | 9      | US-10-013-312-235  | Sequence 235, App  |

|    |    |      |    |                    |                    |
|----|----|------|----|--------------------|--------------------|
| 16 | 27 | 38.0 | 9  | US-10-013-312-512  | Sequence 512, App  |
| 17 | 27 | 38.0 | 9  | US-10-013-312-602  | Sequence 602, App  |
| 18 | 27 | 38.0 | 9  | US-10-013-312-1404 | Sequence 1404, App |
| 19 | 27 | 38.0 | 9  | US-10-013-312-1464 | Sequence 1464, App |
| 20 | 27 | 38.0 | 9  | US-10-013-312-1554 | Sequence 1554, App |
| 21 | 27 | 38.0 | 9  | US-10-013-312-1612 | Sequence 1612, App |
| 22 | 27 | 38.0 | 9  | US-10-013-312-1672 | Sequence 1672, App |
| 23 | 27 | 38.0 | 9  | US-10-013-312-1976 | Sequence 1976, App |
| 24 | 27 | 38.0 | 10 | US-10-013-312-52   | Sequence 52, Appl  |
| 25 | 27 | 38.0 | 10 | US-10-013-312-183  | Sequence 183, App  |
| 26 | 27 | 38.0 | 10 | US-10-013-312-254  | Sequence 254, App  |
| 27 | 27 | 38.0 | 10 | US-10-013-312-384  | Sequence 384, App  |
| 28 | 27 | 38.0 | 10 | US-10-013-312-497  | Sequence 497, App  |
| 29 | 27 | 38.0 | 10 | US-10-013-312-664  | Sequence 664, App  |
| 30 | 27 | 38.0 | 10 | US-10-013-312-686  | Sequence 686, App  |
| 31 | 27 | 38.0 | 10 | US-10-013-312-2094 | Sequence 2094, App |
| 32 | 27 | 38.0 | 10 | US-10-013-312-2114 | Sequence 2114, App |
| 33 | 27 | 38.0 | 10 | US-10-013-312-2217 | Sequence 2217, App |
| 34 | 27 | 38.0 | 10 | US-10-013-312-2250 | Sequence 2250, App |
| 35 | 27 | 38.0 | 10 | US-10-013-312-2321 | Sequence 2321, App |
| 36 | 27 | 38.0 | 10 | US-10-013-312-2339 | Sequence 2339, App |
| 37 | 27 | 38.0 | 10 | US-10-013-312-2407 | Sequence 2407, App |
| 38 | 27 | 38.0 | 10 | US-10-360-101-155  | Sequence 155, App  |
| 39 | 27 | 38.0 | 10 | US-10-360-101-156  | Sequence 156, App  |
| 40 | 27 | 38.0 | 10 | US-10-360-101-157  | Sequence 157, App  |
| 41 | 27 | 38.0 | 10 | US-10-723-434-113  | Sequence 113, App  |
| 42 | 27 | 38.0 | 10 | US-10-723-434-132  | Sequence 132, App  |
| 43 | 27 | 38.0 | 12 | US-10-286-457-132  | Sequence 132, App  |
| 44 | 26 | 36.6 | 8  | US-10-182-252A-200 | Sequence 200, App  |
| 45 | 26 | 36.6 | 8  | US-10-062-710-162  | Sequence 162, App  |

## ALIGNMENTS

RESULT 1  
US-10-394-980-52  
; Sequence 52, Application US/10394980  
; Publication No. US20040005633A1  
; GENERAL INFORMATION:  
; APPLICANT: Vandekerckhove, Joel  
; TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND  
; TITLE OF INVENTION: QUANTITATIVE PROTEOME ANALYSIS, AND USES THEREFOR  
; FILE REFERENCE: VBV-001  
; CURRENT APPLICATION NUMBER: US/10/394,980  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: PCT/EP02/03368  
; PRIOR FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: US60/278,171  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: US60/318,749  
; PRIOR FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US60/323,999  
; PRIOR FILING DATE: 2001-09-20  
; NUMBER OF SEQ ID NOS: 473  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 52  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; OTHER INFORMATION: part of CYPB\_HUMAN (peptidyl-prolyl cis-trans isomerase B)  
US-10-394-980-52

Query Match 63.4%; Score 45; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 HYGPGW 11  
|||||  
Db 1 HYGPGW 6

RESULT 2  
US-10-038-612-168  
; Sequence 168, Application US/10038612  
; Publication No. US20020160478A1  
; GENERAL INFORMATION:  
; APPLICANT: Ben-Sasson, Shmuel A.  
; TITLE OF INVENTION: Short Peptides Which Selectively  
; TITLE OF INVENTION: Modulate the Activity of Protein Kinases  
; FILE REFERENCE: 1242.1029-000 (CMCC-679)  
; CURRENT APPLICATION NUMBER: US/10/038,612  
; CURRENT FILING DATE: 2002-01-08  
; PRIOR APPLICATION NUMBER: US 09/161,094  
; PRIOR FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 168  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MYRISTATE  
; LOCATION: (1)...(0)  
; NAME/KEY: AMIDATION  
; LOCATION: (0)...(13)  
; OTHER INFORMATION: TykB  
; US-10-038-612-168

Query Match 50.7%; Score 36; DB 13; Length 13;  
Best Local Similarity 66.7%; Pred. No. 42;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NFKLKHGP 9  
DB 3 NFKLRAHGP 11

RESULT 3  
US-09-849-092-2  
; Sequence 2, Application US/09849092  
; Publication No. US20030032169A1  
; GENERAL INFORMATION:  
; APPLICANT: Eriksson, Ulf; Simon, Andras; Romert, Anna  
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH  
; TITLE OF INVENTION: CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL DEHYDROGENASE  
; TITLE OF INVENTION: ACTIVITY, AND WHICH ASSOCIATES WITH P63, A PORTION OF A  
; TITLE OF INVENTION: RETINOL BINDING PROTEIN RECEPTOR  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/849,092  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/729,594  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/375,962  
; FILING DATE: 20-January-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/258,418  
; FILING DATE: 10-June-1994

ATTORNEY/AGENT INFORMATION:  
; NAME: Hanson, No. US20030032169A1man D.  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: LUD 5372.3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-849-092-2

Query Match 43.7%; Score 31; DB 10; Length 8;  
Best Local Similarity 80.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 YGPGW 11  
DB 1 YSPGW 5

RESULT 4  
US-09-791-551-99  
; Sequence 99, Application US/09791551  
; Publication No. US20030235584A1  
; GENERAL INFORMATION:  
; APPLICANT: KLOETZER, WILLIAM S.  
; APPLICANT: HANNA, NABIL  
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES  
; FILE REFERENCE: 037003/0277869  
; CURRENT APPLICATION NUMBER: US/09/791,551  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/185,390  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/233,625  
; PRIOR FILING DATE: 2000-09-18  
; NUMBER OF SEQ ID NOS: 119  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 99  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus sp.  
; US-09-791-551-99

Query Match 43.7%; Score 31; DB 11; Length 11;  
Best Local Similarity 66.7%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 HYGPW 11  
DB 2 HYSSW 7

RESULT 5  
US-09-880-748-2870  
; Sequence 2870, Application US/09880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PFS23  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379

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; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2870
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2870
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Query Match      42.3%; Score 30; DB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      8 GPGW 11
      ||||
Db      2 GPGW 5
```

```
RESULT 6
US-10-293-418-2870
; Sequence 2870, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blvs
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2870
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2870
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Query Match      42.3%; Score 30; DB 12; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      8 GPGW 11
      ||||
Db      2 GPGW 5
```

```
RESULT 7
US-10-169-710-23
; Sequence 23, Application US/10169710
; Publication No. US20030181362A1
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS
; TITLE OF INVENTION: HUMAN AND PARASITE ORPHAN RECEPTOR PROTEINS
; FILE REFERENCE: 2551-79
; CURRENT APPLICATION NUMBER: US/10/169,710
; PRIOR FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: PCT/GB01/00085
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; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: GB0000474.7
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 11
; TYPE: PRT
; ORGANISM: shistosoma haematobium
US-10-169-710-23
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Query Match      42.3%; Score 30; DB 14; Length 11;
Best Local Similarity 57.1%; Pred.No. 3.5e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 KLRHYP 9
      ||||
Db      4 KLRHYP 10
```

```
RESULT 8
US-10-038-612-169
; Sequence 169, Application US/10038612
; Publication No. US20020160478A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: Short Peptides Which Selectively
; FILE REFERENCE: 1242.1029-000 (CMCC-679)
; CURRENT APPLICATION NUMBER: US/10/038,612
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 09/161,094
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 169
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MYRISTATE
; LOCATION: (1)..(0)
; NAME/KEY: AMIDATION
; LOCATION: (0)..(13)
; OTHER INFORMATION: TrkB
US-10-038-612-169
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Query Match      42.3%; Score 30; DB 13; Length 13;
Best Local Similarity 62.5%; Pred.No. 4.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 KLRHYP 9
      ||||
Db      2 KLRHYP 9
```

```
RESULT 9
US-10-239-321A-52
; Sequence 52, Application US/10239321A
; Publication No. US20040116336A1
; GENERAL INFORMATION:
; APPLICANT: KITADA, Chieko
; APPLICANT: NISHIZAWA, Naoki
; APPLICANT: HINUMA, Shuji
; APPLICANT: HOSOYA, Masaki
; TITLE OF INVENTION: Peptide derivative
; FILE REFERENCE: 2702 USOP
; CURRENT APPLICATION NUMBER: US/10/239,321A
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: PCT/JP01/02278
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: JP 12-87114
; PRIOR FILING DATE: 2000-03-23
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; PRIOR APPLICATION NUMBER: JP 12-288891  
; PRIOR FILING DATE: 2000-09-19  
; NUMBER OF SEQ ID NOS: 72  
; SEQ ID NO 52  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: peptide derivative  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: Xaa means pGlu  
US-10-239-321A-52

Query Match 42.3%; Score 30; DB 16; Length 13;  
Best Local Similarity 57.1%; Pred. No. 4.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KLKHYGP 9  
|||:  
Db 4 RLSHFGP 10

RESULT 10  
US-10-450-036A-95  
; Sequence 95, Application US/10450036A  
; Publication No. US20040161738A1  
; GENERAL INFORMATION:  
; APPLICANT: MURUGANANDAM, ARUMUGAM  
; APPLICANT: TANHA, JASMID  
; APPLICANT: NARANG, SARAM  
; APPLICANT: STANIMIROVIC, DANICA  
; TITLE OF INVENTION: SINGLE-DOMAIN BRAIN TARGETING ANTIBODY FRAGMENTS  
; TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES  
; FILE REFERENCE: 1339-25  
; CURRENT APPLICATION NUMBER: US/10/450,036A  
; CURRENT FILING DATE: 2004-01-09  
; PRIOR APPLICATION NUMBER: PCT/CA01/00783  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/263,108  
; PRIOR FILING DATE: 2001-01-22  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 95  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Lama glama  
US-10-450-036A-95

Query Match 40.8%; Score 29; DB 16; Length 10;  
Best Local Similarity 55.6%; Pred. No. 4.7e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FKLKHYGPG 10  
|||:  
Db 2 FKITHYTMG 10

RESULT 11  
US-09-910-552-37  
; Sequence 37, Application US/09910552  
; Publication No. US20020197260A1  
; GENERAL INFORMATION:  
; APPLICANT: Granoff, Dan M.  
; APPLICANT: Moe, Gregory R.  
; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE  
; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE  
; TITLE OF INVENTION: COMPOSITIONS  
; FILE REFERENCE: 1238.002  
; CURRENT APPLICATION NUMBER: US/09/910,552  
; CURRENT FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: 09/494,822

; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sequence from  
US-09-910-552-37

Query Match 39.4%; Score 28; DB 9; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKH 6  
|||:  
Db 2 NFKVRH 7

RESULT 12  
US-10-643-465-37  
; Sequence 37, Application US/10643465  
; Publication No. US20040077840A1  
; GENERAL INFORMATION:  
; APPLICANT: Granoff, Dan M.  
; APPLICANT: Moe, Gregory R.  
; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE  
; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE  
; TITLE OF INVENTION: COMPOSITIONS  
; FILE REFERENCE: 1238.002  
; CURRENT APPLICATION NUMBER: US/10/643,465  
; CURRENT FILING DATE: 2003-08-19  
; PRIOR APPLICATION NUMBER: US/08/925,002  
; PRIOR FILING DATE: 1997-08-27  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sequence from  
US-10-643-465-37

Query Match 39.4%; Score 28; DB 16; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NFKLKH 6  
|||:  
Db 2 NFKVRH 7

RESULT 13  
US-10-072-419-2  
; Sequence 2, Application US/10072419  
; Publication No. US20030162717A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Lee  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/072,419  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Gromphadorhina portentosa

US-10-072-419-2

Query Match 39.4%; Score 28; DB 14; Length 10;  
Best Local Similarity 50.0%; Pred. No. 6.9e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYGPGW 11  
Db 3 NPSPGW 8

RESULT 14

US-10-013-312-41  
; Sequence 41, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-41

Query Match 38.0%; Score 27; DB 12; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLKHYG 8  
Db 1 KLEHFG 6

RESULT 15

US-10-013-312-235  
; Sequence 235, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 235  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-235

Query Match 38.0%; Score 27; DB 12; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLKHYG 8

Db 1 KLEHFG 6

RESULT 16

US-10-013-312-512  
; Sequence 512, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 512  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-512

Query Match 38.0%; Score 27; DB 12; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLKHYG 8  
Db 3 KLEHFG 8

RESULT 17

US-10-013-312-602  
; Sequence 602, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 602  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-602

Query Match 38.0%; Score 27; DB 12; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLKHYG 8  
Db 3 KLEHFG 8

RESULT 18

US-10-013-312-1404  
; Sequence 1404, Application US/10013312

```
; Publication No. US2003022390A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIEB USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1404
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1404
```

```
Query Match          38.0%; Score 27; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 KKKHYG 8
        ||:|:|
DB      1 KLEHFG 6
```

```
RESULT 19
US-10-013-312-1464
; Sequence 1464, Application US/10013312
; Publication No. US2003022390A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIEB USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1464
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1464
```

```
Query Match          38.0%; Score 27; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 KKKHYG 8
        ||:|:|
DB      1 KLEHFG 6
```

```
RESULT 20
US-10-013-312-1554
; Sequence 1554, Application US/10013312
; Publication No. US2003022390A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
US-10-013-312-1554
```

```
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIEB USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1554
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1554
```

```
Query Match          38.0%; Score 27; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 KKKHYG 8
        ||:|:|
DB      1 KLEHFG 6
```

```
RESULT 21
US-10-013-312-1612
; Sequence 1612, Application US/10013312
; Publication No. US2003022390A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIEB USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1612
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-1612
```

```
Query Match          38.0%; Score 27; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 KKKHYG 8
        ||:|:|
DB      3 KLEHFG 8
```

```
RESULT 22
US-10-013-312-1672
; Sequence 1672, Application US/10013312
; Publication No. US2003022390A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIEB USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
US-10-013-312-1672
```



SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1672  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-1672

Query Match 38.0%; Score 27; DB 12; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLKHYG 8  
||:|:  
Db 3 KLEHFG 8

## RESULT 23

US-10-013-312-1976  
; Sequence 1976, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193PIEB USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1976  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-1976

Query Match 38.0%; Score 27; DB 12; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLKHYG 8  
||:|:  
Db 3 KLEHFG 8

## RESULT 24

US-10-013-312-52  
; Sequence 52, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193PIEB USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 52  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-52

Query Match 38.0%; Score 27; DB 12; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLKHYG 8  
||:|:  
Db 1 KLEHFG 6

## RESULT 25

US-10-013-312-183  
; Sequence 183, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193PIEB USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 183  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-183

Query Match 38.0%; Score 27; DB 12; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLKHYG 8  
||:|:  
Db 4 KLEHFG 9

## RESULT 26

US-10-013-312-254  
; Sequence 254, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193PIEB USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 254  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-254

Query Match 38.0%; Score 27; DB 12; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLKHYG 8  
||:|:  
Db 1 KLEHFG 6

## RESULT 27

US-10-013-312-384  
; Sequence 384, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA.  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBYVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193PIEB USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 384  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-384

Query Match 38.0%; Score 27; DB 12; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLKHYG 8  
||:|:|  
Db 4 KLEHFG 9

## RESULT 28

US-10-013-312-497  
; Sequence 497, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBYVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193PIEB USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 497  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-497

Query Match 38.0%; Score 27; DB 12; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLKHYG 8  
||:|:|  
Db 4 KLEHFG 9

RESULT 29  
US-10-013-312-664  
; Sequence 664, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:

; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBYVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193PIEB USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 664  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-664

Query Match 38.0%; Score 27; DB 12; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLKHYG 8  
||:|:|  
Db 3 KLEHFG 8

RESULT 30  
US-10-013-312-686  
; Sequence 686, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBYVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; TITLE OF INVENTION: 193PIEB USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 686  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-686

Query Match 38.0%; Score 27; DB 12; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLKHYG 8  
||:|:|  
Db 1 KLEHFG 6

RESULT 31  
US-10-013-312-2094  
; Sequence 2094, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: FARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBYVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED

```
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2094
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2094
```

```
Query Match          38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      3 KLKHYG 8
        ||:|:|
Db      1 KLEHFG 6
```

```
RESULT 32
US-10-013-312-2114
; Sequence 2114, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2114
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2114
```

```
Query Match          38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      3 KLKHYG 8
        ||:|:|
Db      4 KLEHFG 9
```

```
RESULT 33
US-10-013-312-2217
; Sequence 2217, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2217
```

```
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2217
```

```
Query Match          38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      3 KLKHYG 8
        ||:|:|
Db      1 KLEHFG 6
```

```
RESULT 34
US-10-013-312-2250
; Sequence 2250, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2250
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2250
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```
Query Match          38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      3 KLKHYG 8
        ||:|:|
Db      1 KLEHFG 6
```

```
RESULT 35
US-10-013-312-2321
; Sequence 2321, Application US/10013312
; Publication No. US20030223990A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 193PIE1B USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20063.00
; CURRENT APPLICATION NUMBER: US/10/013,312
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 3005
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2321
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-312-2321
```

```
Query Match          38.0%; Score 27; DB 12; Length 10;
Best Local Similarity 66.7%; Pred. No. 1e+03;
```

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KLKHYG 8  
|:|:|  
Db 4 KLEHFG 9

RESULT 36  
US-10-013-312-2339  
; Sequence 2339, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AVA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2339  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-2339

Query Match 38.0%; Score 27; DB 12; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLKHYG 8  
|:|:|  
Db 1 KLEHFG 6

RESULT 37  
US-10-013-312-2407.  
; Sequence 2407, Application US/10013312  
; Publication No. US20030223990A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: PARIS, MARY  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AVA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED  
; FILE REFERENCE: 51158-20063.00  
; CURRENT APPLICATION NUMBER: US/10/013,312  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 3005  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2407  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-013-312-2407

Query Match 38.0%; Score 27; DB 12; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KLKHYG 8  
|:|:|  
Db 5 KLEHFG 10

RESULT 38  
US-10-360-101-155  
; Sequence 155, Application US/10360101  
; Publication No. US20040009550A1  
; GENERAL INFORMATION:  
; APPLICANT: MOLL, GERT N.  
; APPLICANT: LEENHOUTS, CORNELIS J.  
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way  
; FILE REFERENCE: 2183-5673  
; CURRENT APPLICATION NUMBER: US/10/360,101  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: EP 02077060.8  
; PRIOR FILING DATE: 2002-05-24  
; NUMBER OF SEQ ID NOS: 309  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 155  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: (Q1,A4,S5,C8)-sequence of LHRH2  
US-10-360-101-155

Query Match 38.0%; Score 27; DB 15; Length 10;  
Best Local Similarity 42.9%; Pred. No. 1e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYGPGW 11  
|:|:|  
Db 1 QHWASGW 7

RESULT 39  
US-10-360-101-156  
; Sequence 156, Application US/10360101  
; Publication No. US20040009550A1  
; GENERAL INFORMATION:  
; APPLICANT: MOLL, GERT N.  
; APPLICANT: LEENHOUTS, CORNELIS J.  
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way  
; FILE REFERENCE: 2183-5673  
; CURRENT APPLICATION NUMBER: US/10/360,101  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: EP 02077060.8  
; PRIOR FILING DATE: 2002-05-24  
; NUMBER OF SEQ ID NOS: 309  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 156  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: (Q1,A4,S5,C9)-sequence of LHRH2  
US-10-360-101-156

Query Match 38.0%; Score 27; DB 15; Length 10;  
Best Local Similarity 42.9%; Pred. No. 1e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYGPGW 11  
|:|:|  
Db 1 QHWASGW 7

RESULT 40  
US-10-360-101-157  
; Sequence 157, Application US/10360101  
; Publication No. US20040009550A1  
; GENERAL INFORMATION:  
; APPLICANT: MOLL, GERT N.  
; APPLICANT: LEENHOUTS, CORNELIS J.  
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way  
; FILE REFERENCE: 2183-5673  
US-10-360-101-157

```
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 157
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: (Q1,A4,S5,C10)-sequence of LHRH2
US-10-360-101-157
```

```
Query Match          38.0%; Score 27; DB 15; Length 10;
Best Local Similarity 42.9%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 KHYGPGW 11
      :||:|
Db      1 QHWASGW 7
```

```
RESULT 41
US-10-723-434-113
; Sequence 113, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 113
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH/CDR1
US-10-723-434-113
```

```
Query Match          38.0%; Score 27; DB 16; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 FKLKHYG 8
      :||:|
Db      2 YSLDHYG 8
```

```
RESULT 42
US-10-723-434-132
; Sequence 132, Application US/10723434
; Publication No. US20040133357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark
```

```
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709.501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH/CDR1
US-10-723-434-132
```

```
Query Match          38.0%; Score 27; DB 16; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 FKLKHYG 8
      :||:|
Db      2 YDSLHYG 8
```

```
RESULT 43
US-10-286-457-132
; Sequence 132, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GSCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-132
```

```
Query Match          38.0%; Score 27; DB 14; Length 12;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 NFKLKHYP 9
      :||:|
Db      4 NYKIRSGP 12
```

```
RESULT 44
US-10-182-252A-200
; Sequence 200, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUIS, SOREN
; APPLICANT: CORBET, SYLVIE
```

; APPLICANT: LAUEMOLLER, SANNE LISE  
; APPLICANT: HANSEN, JAN  
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS  
; FILE REFERENCE: 030307/0205  
; CURRENT APPLICATION NUMBER: US/10/182,252A  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: EP 00610017.6  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/179,333  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 1388  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 200  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-200

Query Match 36.6%; Score 26; DB 12; Length 8;  
Best Local Similarity 80.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYPG 10  
| | | |  
Db 1 HIGPG 5

RESULT 45  
US-10-062-710-162  
; Sequence 162, Application US/10062710  
; Publication No. US20030049253A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Frank Q.  
; APPLICANT: Chu, Yong-Liang  
; APPLICANT: Qiu, Jian-Tai  
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of  
; TITLE OF INVENTION: MHC-Recognized Epitopes  
; TITLE OF INVENTION: Via Peptide Vaccines  
; FILE REFERENCE: 3781-001-27  
; CURRENT APPLICATION NUMBER: US/10/062,710  
; CURRENT FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: US 60/310,498  
; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 232  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 162  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV B Cell Epitopes  
US-10-062-710-162

Query Match 36.6%; Score 26; DB 14; Length 8;  
Best Local Similarity 80.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYPG 10  
| | | |  
Db 3 HIGPG 7

Search completed: August 30, 2004, 11:04:57  
Job time : 14.4527 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 4.34797 Seconds  
(without alignments)  
130.609 Million cell updates/sec

Title: US-09-720-469A-5  
Perfect score: 71  
Sequence: 1 NFKLKHYPGW 11

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                              |
|------------|-------|-------------|--------|-------|--|
| 1          | 37    | 52.1        | 14     | 5     | PCT-US93-06751-120<br>Sequence 120, App  |
| 2          | 35    | 49.3        | 9      | 1     | US-07-963-324-2<br>Sequence 2, Appli     |
| 3          | 32    | 45.1        | 14     | 5     | PCT-US93-06751-67<br>Sequence 67, Appl   |
| 4          | 31    | 43.7        | 8      | 1     | US-08-375-9628-2<br>Sequence 2, Appli    |
| 5          | 31    | 43.7        | 8      | 2     | US-08-562-114B-2<br>Sequence 2, Appli    |
| 6          | 31    | 43.7        | 8      | 3     | US-08-729-594A-2<br>Sequence 2, Appli    |
| 7          | 31    | 43.7        | 8      | 4     | US-08-937-993-2<br>Sequence 2, Appli     |
| 8          | 30    | 42.3        | 8      | 1     | US-08-271-830-56<br>Sequence 56, Appl    |
| 9          | 30    | 42.3        | 13     | 5     | PCT-US93-06751-66<br>Sequence 66, Appl   |
| 10         | 30    | 42.3        | 14     | 5     | PCT-US93-06751-93<br>Sequence 93, Appl   |
| 11         | 29    | 40.8        | 10     | 1     | US-08-353-400-26<br>Sequence 26, Appl    |
| 12         | 29    | 40.8        | 14     | 5     | PCT-US93-06751-65<br>Sequence 65, Appl   |
| 13         | 29    | 40.8        | 14     | 5     | PCT-US93-06751-103<br>Sequence 103, Appl |
| 14         | 28    | 39.4        | 8      | 3     | US-08-925-002-37<br>Sequence 37, Appl    |
| 15         | 28    | 39.4        | 8      | 4     | US-09-910-552-37<br>Sequence 37, Appl    |
| 16         | 28    | 39.4        | 10     | 2     | US-08-747-137-122<br>Sequence 122, App   |
| 17         | 28    | 39.4        | 11     | 2     | US-08-598-873-68<br>Sequence 68, Appl    |
| 18         | 28    | 39.4        | 11     | 3     | US-08-605-430-68<br>Sequence 68, Appl    |
| 19         | 28    | 39.4        | 14     | 5     | PCT-US93-06751-63<br>Sequence 63, Appl   |
| 20         | 28    | 39.4        | 14     | 5     | PCT-US93-06751-104<br>Sequence 104, App  |
| 21         | 27    | 38.0        | 9      | 3     | US-08-159-339A-391<br>Sequence 391, App  |
| 22         | 27    | 38.0        | 13     | 5     | PCT-US93-06751-102<br>Sequence 102, App  |
| 23         | 26    | 36.6        | 8      | 1     | US-08-279-906A-5<br>Sequence 5, Appli    |
| 24         | 26    | 36.6        | 8      | 5     | PCT-US92-06688-8<br>Sequence 8, Appli    |
| 25         | 26    | 36.6        | 9      | 1     | US-08-318-970B-23<br>Sequence 23, Appl   |
| 26         | 26    | 36.6        | 9      | 3     | US-08-946-525-4<br>Sequence 4, Appli     |
| 27         | 26    | 36.6        | 9      | 3     | US-09-082-279B-920<br>Sequence 920, App  |

|    |    |      |    |   |   |
|----|----|------|----|---|---|
| 28 | 26 | 36.6 | 9  | 4 | US-09-315-304B-920<br>Sequence 920, App |
| 29 | 26 | 36.6 | 9  | 4 | US-09-599-286-4<br>Sequence 4, Appli    |
| 30 | 26 | 36.6 | 9  | 4 | US-09-834-784-920<br>Sequence 920, App  |
| 31 | 26 | 36.6 | 9  | 4 | US-09-515-965A-920<br>Sequence 920, App |
| 32 | 26 | 36.6 | 9  | 4 | US-09-350-641C-920<br>Sequence 920, App |
| 33 | 26 | 36.6 | 10 | 1 | US-08-250-789A-94<br>Sequence 94, Appl  |
| 34 | 26 | 36.6 | 10 | 1 | US-08-341-219-15<br>Sequence 15, Appl   |
| 35 | 26 | 36.6 | 10 | 1 | US-08-341-219-16<br>Sequence 16, Appl   |
| 36 | 26 | 36.6 | 10 | 1 | US-08-253-030-23<br>Sequence 23, Appl   |
| 37 | 26 | 36.6 | 10 | 1 | US-08-253-030-25<br>Sequence 25, Appl   |
| 38 | 26 | 36.6 | 10 | 1 | US-08-425-069-19<br>Sequence 19, Appl   |
| 39 | 26 | 36.6 | 10 | 2 | US-08-687-559-10<br>Sequence 10, Appl   |
| 40 | 26 | 36.6 | 10 | 2 | US-08-317-844B-19<br>Sequence 19, Appl  |
| 41 | 26 | 36.6 | 10 | 3 | US-08-946-525-15<br>Sequence 15, Appl   |
| 42 | 26 | 36.6 | 10 | 3 | US-08-912-314A-15<br>Sequence 15, Appl  |
| 43 | 26 | 36.6 | 10 | 3 | US-08-912-314A-16<br>Sequence 16, Appl  |
| 44 | 26 | 36.6 | 10 | 4 | US-09-599-286-15<br>Sequence 15, Appl   |
| 45 | 26 | 36.6 | 10 | 4 | US-09-401-415-10<br>Sequence 10, Appl   |

ALIGNMENTS

RESULT 1  
PCT-US93-06751-120  
Sequence 120, Application PC/TUS9306751  
GENERAL INFORMATION:  
APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold  
TITLE OF INVENTION: Immunological Conjugates of OMPC and  
TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GxG Epitopes  
NUMBER OF SEQUENCES: 146  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06751  
FILING DATE: 19930719  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meredith, Roy D.  
REGISTRATION NUMBER: 30,777  
REFERENCE/DOCKET NUMBER: 18614  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-4678  
TELEFAX: (908) 594-4720  
TELEX: 138825  
INFORMATION FOR SEQ ID NO: 120:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE: Random Epitope Library Beta  
PCT-US93-06751-120

Query Match 52.1% Score 37; DB 5; Length 14;  
Best Local Similarity 55.6% Pred. No. 6.2;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 2 FKLKHYPG 10  
:: |||||

Db 3 YRAHYGPG 11

## RESULT 2

US-07-963-324-2

; Sequence 2, Application US/07963324  
; Patent No. 5274122

## GENERAL INFORMATION:

APPLICANT: Marburg, Stephen  
APPLICANT: Leanza, William J  
APPLICANT: Tolman, Richard L  
TITLE OF INVENTION: Acidic Derivatives of Homocysteine  
TITLE OF INVENTION: Thiolactone  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: 126 Lincoln Avenue  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07065

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/963,324  
FILING DATE: 19921015

## CLASSIFICATION: 530

## ATTORNEY/AGENT INFORMATION:

NAME: Bencen, Gerard H  
REGISTRATION NUMBER: 35,746  
REFERENCE/DOCKET NUMBER: 18787  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)594-3901  
TELEFAX: (908)594-4720

## INFORMATION FOR SEQ ID NO: 2:

## SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: AMINO ACID

TOPOLOGY: both

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

## FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /label= Nle

OTHER INFORMATION: /note= "norleucine"

## FEATURE:

NAME/KEY: Cross-links

LOCATION: 2..9

OTHER INFORMATION: /label= cycle

OTHER INFORMATION: /note= "amide bond through lys epsilon amino"

US-07-963-324-2

## Query Match

Best Local Similarity 49.3%; Score 35; DB 1; Length 9;  
85.7%; Pred. No. 3e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LKHGPG 10

DB 1 LKHGPG 7

## RESULT 3

PCT-US93-06751-67

; Sequence 67, Application PC/TUS9306751

## GENERAL INFORMATION:

APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold  
TITLE OF INVENTION: Immunological Conjugates of OMPC and

TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes

NUMBER OF SEQUENCES: 146

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck &amp; Co., Inc.

STREET: P.O. Box 2000

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/06751

FILING DATE: 19930719

## CLASSIFICATION:

## ATTORNEY/AGENT INFORMATION:

NAME: Meredith, Roy D.

REGISTRATION NUMBER: 30,777

REFERENCE/DOCKET NUMBER: 18614

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-4678

TELEFAX: (908) 594-4720

TELEX: 138825

INFORMATION FOR SEQ ID NO: 67:

## SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

IMMEDIATE SOURCE: Random Epitope Library Gamma

PCT-US93-06751-67

## Query Match

Best Local Similarity 45.1%; Score 32; DB 5; Length 14;  
71.4%; Pred. No. 42;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KLKHYGP 9

DB 1 KANHYGP 7

## RESULT 4

US-08-375-962B-2

; Sequence 2, Application US/08375962B

; Patent No. 5731195

## GENERAL INFORMATION:

APPLICANT: SIMON, ANDRAS; HELLMAN, ULF; WERNSTEDT,

APPLICANT: CHRISTER, ERIKSSON, ULF.

TITLE OF INVENTION: Isolated Nucleic Acid Molecule

TITLE OF INVENTION: Which Codes for A 32 kDa Protein Having 11-CIS Retinol

TITLE OF INVENTION: Dehydrogenase Activity, and Which Associates With P63,

TITLE OF INVENTION: a Portion of a Retinol Binding Protein Receptor

NUMBER OF SEQUENCES: 14

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Felte &amp; Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

ZIP: 10022

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect (ASCII standard)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/375,962B

FILING DATE: 20-January-1995



```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/258,418
; FILING DATE: 6-October-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5372.1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-375-962B-2

```

```

Query Match      43.7%; Score 31; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      7 YGPGW 11
      1 |||
Db      1 YSPGW 5

```

RESULT 5

```

US-08-562-114B-2
; Sequence 2, Application US/08562114B
; Patent No. 5972646
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON ET AL.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH CODES FOR A
; TITLE OF INVENTION: 32 KDA PROTEIN HAVING 11-CIS RETINOL HYDROGENASE
; TITLE OF INVENTION: ACTIVITY, AND WHICH ASSOCIATES WITH P63, A
; TITLE OF INVENTION: PORTION OF A RETINOL BINDING PROTEIN RECEPTOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felife & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect 5.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/562,114B
; FILING DATE: 22-No. 5972646ember-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/375,962
; FILING DATE: 20-January-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohl, Vineet
; REGISTRATION NUMBER: 37,003
; REFERENCE/DOCKET NUMBER: LUD 5372.2 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-562-114B-2

```

```

Query Match      43.7%; Score 31; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      7 YGPGW 11
      1 |||
Db      1 YSPGW 5

```

RESULT 6

```

US-08-729-594A-2
; Sequence 2, Application US/08729594A
; Patent No. 6280997
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Ulf, Simon, Andras, Romert, Anna
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH
; TITLE OF INVENTION: CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL DEHYDROGENASE
; TITLE OF INVENTION: ACTIVITY, AND WHICH ASSOCIATES WITH P63, A PORTION OF A
; TITLE OF INVENTION: RETINOL BINDING PROTEIN RECEPTOR
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felife & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,594A
; FILING DATE: 11-October-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/562,114
; FILING DATE: 22-No. 6280997ember-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/375,962
; FILING DATE: 20-January-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/258,418
; FILING DATE: 10-June-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 628097man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5372.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-729-594A-2

```

```

Query Match      43.7%; Score 31; DB 3; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      7 YGPGW 11
      1 |||
Db      1 YSPGW 5

```

RESULT 7

```

US-08-937-993-2
; Sequence 2, Application US/08937993
; Patent No. 639344
; GENERAL INFORMATION:

```

APPLICANT: Eriksson, Ulf, Simon, Andras; Romert, Anna  
TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fulbright & Jaworski L.L.P.  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/937,993  
FILING DATE: September 26, 1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/729,594  
FILING DATE: 11-October-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/562,114  
FILING DATE: 22-No. 6399344ember-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/375,962  
FILING DATE: 20-January-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/258,418  
FILING DATE: 10-June-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6399344man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5517  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-937-993-2

Query Match 43.7%; Score 31; DB 4; Length 8;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 YPGW 11  
| | | |  
Db 1 YSPGW 5

RESULT 8  
US-08-271-830-56  
Sequence 56, Application US/08271830  
Patent No. 5510332  
GENERAL INFORMATION:  
APPLICANT: Kogan, Timothy P.  
APPLICANT: Ren, Kaijun  
APPLICANT: Vanderslice, Peter  
APPLICANT: Beck, Pamela J.  
TITLE OF INVENTION: A PROCESS OF INHIBITING THE BINDING OF THE  
TITLE OF INVENTION: INTEGRIN '4 1 TO VCAM OR FIBRONECTIN AND  
TITLE OF INVENTION: LINEAR PEPTIDES THEREFOR  
NUMBER OF SEQUENCES: 102  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.  
STREET: 180 No. 5510332th Stetson, Suite 4700  
CITY: Chicago  
STATE: IL

COUNTRY: USA  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/271,830  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5510332thrup, Thomas E.  
REGISTRATION NUMBER: 33,268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312)616-5400  
TELEFAX: (312)616-5460  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 8  
OTHER INFORMATION: /label= Xaa  
OTHER INFORMATION: /note= "Xaa=Pro-NH2."  
US-08-271-830-56

Query Match 42.3%; Score 30; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GPGW 11  
| | | |  
Db 1 GPGW 4

RESULT 9  
PCT-US93-06751-66  
Sequence 66, Application PC/TUS9306751  
GENERAL INFORMATION:  
APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold  
TITLE OF INVENTION: Immunological Conjugates of OMPC and  
TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes  
NUMBER OF SEQUENCES: 146  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06751  
FILING DATE: 19930719  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meredith, Roy D.  
REGISTRATION NUMBER: 30,777  
REFERENCE/DOCKET NUMBER: 18614  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-4678  
TELEFAX: (908) 594-4720  
TELEX: 138825  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 IMMEDIATE SOURCE: Random Epitope Library Delta  
 PCT-US93-06751-66

Query Match 42.3%; Score 30; DB 5; Length 13;  
 Best Local Similarity 80.0%; Pred. No. 86;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HYPG 10  
 Db 4 HFGPG 8

RESULT 10

PCT-US93-06751-93  
 ; Sequence 93, Application PC/TUS9306751  
 ; GENERAL INFORMATION:  
 ; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold  
 ; TITLE OF INVENTION: Immunological Conjugates of OMPC and  
 ; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes  
 ; NUMBER OF SEQUENCES: 146  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Merck & Co., Inc.  
 ; STREET: P.O. Box 2000  
 ; CITY: Rahway  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07065  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US93/06751  
 ; FILING DATE: 19930719  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Meredith, Roy D.  
 ; REGISTRATION NUMBER: 30,777  
 ; REFERENCE/DOCKET NUMBER: 18614  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (908) 594-4678  
 ; TELEFAX: (908) 594-4720  
 ; TELEX: 138825  
 ; INFORMATION FOR SEQ ID NO: 93:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 14 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; IMMEDIATE SOURCE: Random Epitope Library Gamma  
 ; PCT-US93-06751-93

Query Match 42.3%; Score 30; DB 5; Length 14;  
 Best Local Similarity 80.0%; Pred. No. 92;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HYPG 10  
 Db 4 HFGPG 8

RESULT 11

US-08-353-400-26  
 ; Sequence 26, Application US/08353400  
 ; Patent No. 565357  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: PROTEINS  
 ; NUMBER OF SEQUENCES: 37  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/353,400  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 9324819.3  
 ; FILING DATE: 03-DEC-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 9411089.7  
 ; FILING DATE: 03-JUN-1994  
 ; INFORMATION FOR SEQ ID NO: 26:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-353-400-26

Query Match 40.8%; Score 29; DB 1; Length 10;  
 Best Local Similarity 57.1%; Pred. No. 98;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 KHYPGW 11  
 Db 3 EHRGSGW 9

RESULT 12

PCT-US93-06751-65  
 ; Sequence 65, Application PC/TUS9306751  
 ; GENERAL INFORMATION:  
 ; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold  
 ; TITLE OF INVENTION: Immunological Conjugates of OMPC and  
 ; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes  
 ; NUMBER OF SEQUENCES: 146  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Merck & Co., Inc.  
 ; STREET: P.O. Box 2000  
 ; CITY: Rahway  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07065  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US93/06751  
 ; FILING DATE: 19930719  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Meredith, Roy D.  
 ; REGISTRATION NUMBER: 30,777  
 ; REFERENCE/DOCKET NUMBER: 18614  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (908) 594-4678  
 ; TELEFAX: (908) 594-4720  
 ; TELEX: 138825  
 ; INFORMATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE: Random Epitope Library Delta  
PCT-US93-06751-65

Query Match 40.8%; Score 29; DB 5; Length 14;  
Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 HYGP 10  
: : : :  
Db 4 HWGP 8

## RESULT 13

PCT-US93-06751-103  
Sequence 103, Application PC/TUS9306751

GENERAL INFORMATION:  
APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold  
TITLE OF INVENTION: Immunological Conjugates of OMPC and  
TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes  
NUMBER OF SEQUENCES: 146  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06751  
FILING DATE: 19930719  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meredith, Roy D.  
REGISTRATION NUMBER: 30,777  
REFERENCE/DOCKET NUMBER: 18614  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-4678  
TELEFAX: (908) 594-4720  
TELEX: 138825  
INFORMATION FOR SEQ ID NO: 103:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE: Random Epitope Library Delta  
PCT-US93-06751-103

Query Match 40.8%; Score 29; DB 5; Length 14;  
Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 KLKHYGP 10  
: : : :  
Db 1 EVHYGP 8

## RESULT 14

US-08-925-002-37  
Sequence 37, Application US/08925002  
Patent No. 6048527  
GENERAL INFORMATION:  
APPLICANT: Granoff, Dan M.  
TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE  
TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE  
TITLE OF INVENTION: COMPOSITIONS  
FILE REFERENCE: 1238.002  
CURRENT APPLICATION NUMBER: US/08/925.002  
CURRENT FILING DATE: 1997-08-27  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 37  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: sequence from  
US-08-925-002-37

Query Match 39.4%; Score 28; DB 3; Length 8;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 NFKLKH 6  
: : : :  
Db 2 NFKVRH 7

## RESULT 15

US-09-910-552-37  
Sequence 37, Application US/09910552  
Patent No. 6642354  
GENERAL INFORMATION:  
APPLICANT: Granoff, Dan M.  
TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE  
TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE  
TITLE OF INVENTION: COMPOSITIONS  
FILE REFERENCE: 1238.002  
CURRENT APPLICATION NUMBER: US/09/910.552  
CURRENT FILING DATE: 2001-07-23  
PRIOR APPLICATION NUMBER: 09/494,822  
PRIOR FILING DATE: 2000-01-31  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 37  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: sequence from  
US-09-910-552-37

Query Match 39.4%; Score 28; DB 4; Length 8;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 NFKLKH 6  
: : : :  
Db 2 NFKVRH 7

## RESULT 16

US-08-747-137-122  
Sequence 122, Application US/08747137  
Patent No. 5945033  
GENERAL INFORMATION:

APPLICANT: YEN, Richard C.K.  
TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR  
THERAPEUTIC AND DIAGNOSTIC USE  
NUMBER OF SEQUENCES: 184  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,137  
FILING DATE: 12-NOV-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/212,546  
FILING DATE: 14-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/069,831  
FILING DATE: 01-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/959,560  
FILING DATE: 13-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/641,720  
FILING DATE: 15-JAN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 016197-000840US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
INFORMATION FOR SEQ ID NO: 122:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "p-Glu"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: /product= "Thr-Amide"  
US-08-747-137-122

Query Match 39.4%; Score 28; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYPGW 11  
: : : :  
Db 3 NPSPGW 8

RESULT 17  
US-08-598-873-68  
Sequence 68, Application US/08598873  
Patent No. 5928884  
GENERAL INFORMATION:  
APPLICANT: Croce, Carlo M.  
ATTORNEY/AGENT INFORMATION:  
NAME: Huebner, Kay  
REGISTRATION NUMBER: 29,258  
REFERENCE/DOCKET NUMBER: 8666-005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/598,873  
FILING DATE: 09-FEB-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Friebe, Thomas E.  
REGISTRATION NUMBER: 29,258  
REFERENCE/DOCKET NUMBER: 8666-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-598-873-68

Query Match 39.4%; Score 28; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HYPG 9  
: : : :  
Db 1 HYPG 4

RESULT 18  
US-08-605-430-68  
Sequence 68, Application US/08605430  
Patent No. 6242212  
GENERAL INFORMATION:  
APPLICANT: Croce, Carlo M.  
ATTORNEY/AGENT INFORMATION:  
NAME: Huebner, Kay  
REGISTRATION NUMBER: 29,258  
REFERENCE/DOCKET NUMBER: 8666-005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090

Query Match 39.4%; Score 28; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HYPG 9  
: : : :  
Db 1 HYPG 4

RESULT 18  
US-08-605-430-68  
Sequence 68, Application US/08605430  
Patent No. 6242212  
GENERAL INFORMATION:  
APPLICANT: Croce, Carlo M.  
ATTORNEY/AGENT INFORMATION:  
NAME: Huebner, Kay  
REGISTRATION NUMBER: 29,258  
REFERENCE/DOCKET NUMBER: 8666-005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-605-430-68

Query Match 39.4%; Score 28; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 HYPG 9  
Db 1 HYPG 4

## RESULT 19

PCT-US93-06751-63  
Sequence 63, Application PC/TUS9306751

GENERAL INFORMATION:  
APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold  
TITLE OF INVENTION: Immunological Conjugates of OMPC and  
TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GxG Epitopes  
NUMBER OF SEQUENCES: 146  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06751  
FILING DATE: 19930719  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meredith, Roy D.  
REGISTRATION NUMBER: 30,777  
REFERENCE/DOCKET NUMBER: 18614  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-4678  
TELEFAX: (908) 594-4720  
TELEX: 138825

INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE: Random Epitope Library Delta  
PCT-US93-06751-63

Query Match 39.4%; Score 28; DB 5; Length 14;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHYGPG 10  
Db 3 RHLGPG 8

## RESULT 20

PCT-US93-06751-104

Sequence 104, Application PC/TUS9306751  
GENERAL INFORMATION:

APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold  
TITLE OF INVENTION: Immunological Conjugates of OMPC and  
TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GxG Epitopes  
NUMBER OF SEQUENCES: 146  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06751  
FILING DATE: 19930719  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meredith, Roy D.  
REGISTRATION NUMBER: 30,777  
REFERENCE/DOCKET NUMBER: 18614  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-4678  
TELEFAX: (908) 594-4720  
TELEX: 138825

INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE: Random Epitope Library Delta  
PCT-US93-06751-104

Query Match 39.4%; Score 28; DB 5; Length 14;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHYGPG 10  
Db 3 RHLGPG 8

## RESULT 21

US-08-159-339A-391  
Sequence 391, Application US/08159339A

Patent No. 6037135  
GENERAL INFORMATION:

APPLICANT: Kubo, Ralph T.  
APPLICANT: Grey, Howard M.  
APPLICANT: Sette, Alessandro  
APPLICANT: Celis, Esteban  
TITLE OF INVENTION: HLA Binding peptides and Their  
NUMBER OF SEQUENCES: 1254  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

```

; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 391:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-391

Query Match      38.0%; Score 27; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 FKLKHY 7
      |||
Db      3 FKTRHY 8

RESULT 22
PCT-US93-06751-102
; Sequence 102, Application PC/TUS9306751
; GENERAL INFORMATION:
; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
; TITLE OF INVENTION: Immunological Conjugates of OMPC and
; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06751
; FILING DATE: 19930719
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: 18614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4678
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 102:
```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE: Random Epitope Library Delta
; PCT-US93-06751-102

Query Match      38.0%; Score 27; DB 5; Length 13;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 HYGP 10
      |||
Db      4 NYGP 8

RESULT 23
US-08-279-906A-5
; Sequence 5, Application US/08279906A
; Patent No. 5618922
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; APPLICANT: Terada, Masaki
; APPLICANT: Yoneda, Yukio
; TITLE OF INVENTION: NM03 Antibody Materials and Methods
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/279,906A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5618922and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-279-906A-5

Query Match      36.6%; Score 26; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 HYGP 10
      |||
Db      1 HIGP 5

RESULT 24
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PCT-US92-06688-8  
; Sequence 8, Application PC/TUS9206688  
; GENERAL INFORMATION:  
; APPLICANT: REPLIGEN CORPORATION  
; TITLE OF INVENTION: THE ROCKEFELLER UNIVERSITY  
; TITLE OF INVENTION: MULTIPLE ANTIGEN PEPTIDES FOR USE AS HIV  
; TITLE OF INVENTION: VACCINES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/06688  
; FILING DATE: 19920811  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 744,281  
; FILING DATE: 13 August 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul T. Clark  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00231/052W01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; PCT-US92-06688-8

Query Match 36.6%; Score 26; DB 5; Length 8;  
Best Local Similarity 80.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HYPG 10  
| | |  
Db 3 HIGPG 7

RESULT 25  
US-08-318-970B-23  
; Sequence 23, Application US/08318970B  
; Patent No. 5589573  
; GENERAL INFORMATION:  
; APPLICANT: Hideaki HAGIMARA, et al.  
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC  
; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY  
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Office of Sherman and Shalloway  
; STREET: 413 N. Washington Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor  
; OPERATING SYSTEM: MS DOS 3.3  
; SOFTWARE: Word Perfect, Version 5.1

CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/318,970B  
; FILING DATE: October 6, 1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Richard A. Steindberg  
; REGISTRATION NUMBER: 26,588  
; REFERENCE/DOCKET NUMBER: S-2371  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 549-2282  
; TELEFAX: (703) 836-0106  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: L CDR3-5  
; OTHER INFORMATION: hypervariable region.  
; US-08-318-970B-23

Query Match 36.6%; Score 26; DB 1; Length 9;  
Best Local Similarity 42.9%; Pred. No. 3e+05;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KHYPGW 11  
: | |  
Db 2 QHYSTAW 8

RESULT 26  
US-08-946-525-4  
; Sequence 4, Application US/08946525  
; Patent No. 6139843  
; GENERAL INFORMATION:  
; APPLICANT: Arye Rubinstein, Barry R. Bloom, Yair Devash and Stanley J. Cryz  
; TITLE OF INVENTION: PEPTIDE COMPOSITIONS FOR THE TREATMENT AND  
; TITLE OF INVENTION: PREVENTION OF HIV  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amster, Rothenstein & Ebenstein  
; STREET: 90 Park Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Word Processor (ASCII)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/946,525  
; FILING DATE: October 7, 1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/785,696  
; FILING DATE: January 17, 1997  
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; TELEX: TWX 710-581-4766  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear